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(54) Title: **GENE EXPRESSION PROFILES IN ESOPHAGEAL TISSUE**

(57) Abstract: The present invention results from the examination of tissue from esophageal adenocarcinomas to identify genes differentially expressed between tumor biopsies and normal tissue. The invention includes diagnostic and screening methods using these genes as well as solid supports comprising oligonucleotide arrays that are complementary to or hybridize to the differentially expressed genes.

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GENE EXPRESSION PROFILES IN ESOPHAGEAL TISSUE

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BACKGROUND OF THE INVENTION

There are two main types of esophageal cancer; squamous cell carcinoma (SCC) and adenocarcinoma. The worldwide incidence of esophageal SCC is higher than that of adenocarcinoma; however, in the last few decades, the incidence of adenocarcinoma in Western countries has been increasing at a dramatic rate. As a result, esophageal adenocarcinoma is the most common cancer type among Caucasian patients in some populations (Blot & McLaughlin, *Semin. Oncol.* (1999) 26, 2-8).

The main risk factor for development of esophageal adenocarcinoma is the presence of Barrett's esophagus, a disease in which the normal squamous epithelium of the lower esophagus is replaced by columnar mucosa in response to injury caused by chronic gastroesophageal reflux (Lagergren *et al.*, *N. Engl. J. Med.* (1999) 340, 825-831; Barrett *et al.*, *Nat. Genet.* (1999) 22, 106-109; Reid & Weinstein, *Annu. Rev. Med.* (1987) 38, 477-492). Barrett's esophagus is a disorder in which the lining of the esophagus undergoes cellular changes in response to chronic irritation and inflammation of reflux esophagitis. This condition is more common in men than women. The patient with Barrett's esophagus is at an increased risk of developing cancer of the esophagus. Symptoms are similar to those of reflux esophagitis and include heartburn, difficulty swallowing and pain relief with antacid use or eating. The diagnosis of Barrett's is made by a biopsy of the esophageal mucosa through an endoscope. Treatment includes control of reflux disease, weight reduction and avoidance of alcohol, tobacco, fatty foods and lying flat after eating. Close follow-up is recommended to be certain the individual does not develop cancer of the esophagus.

The precursor cell for Barrett's epithelium has not been identified, leaving the origin of Barrett's esophagus open to speculation. One theory suggests that denudation of the squamous epithelium layer by reflux acid allows gastric columnar cells to move into the site and take over (Bremner *et al.*, *Surgery* (1970) 68, 209-16). More recently, cytokeratin expression data has been used to suggest that Barrett's epithelium evolves from a basal cell in the esophageal squamous epithelium (Boch *et al.*, *Gastroenterology* (1997) 112, 760-765; Salo *et al.*, *Ann. Med.* (1996) 28, 305-309).

The advent of cDNA and oligonucleotide arrays has enabled researchers to map tissue-specific expression levels for thousands of genes (Alon *et al.*, Proc. Natl. Acad. Sci. USA (1999) 96, 6745-6750; Iyer *et al.*, (1999) Science 283, 83-87; Khan *et al.*, Cancer Res. (1998) 58, 5009-13; Lee *et al.*, Science (1999) 285, 1390-1393; Wang *et al.* Gene (1999) 229, 101-108; Whitney *et al.*, Ann. Neurol. (1999) 46, 425-428). Instead of assigning individual genes to a disease phenotype, expression profiles can be created which identify changes in total gene expression in the diseased tissue in relationship to normal adjacent tissue. Present day cancer research, particularly research in the field of adenocarcinoma, has focused on the determining the expression levels of individual genes with little effort expended on determining the global changes in gene expression that are correlated with the development and progression of adenocarcinoma.

There remains a need in the art for materials and methods that permit a more accurate diagnosis of esophageal cancer and, in particular, esophageal adenocarcinoma. In addition, there remains a need in the art for methods to treat and methods to identify agent that can effectively treat esophageal cancer. The present invention meets these and other needs.

SUMMARY OF THE INVENTION

The present invention is based in part on the global changes in gene expression associated with esophageal cancer identified by examining gene expression in tissue from normal and diseased esophagus. The present invention also includes expression profiles which serve as useful diagnostic markers as well as markers that can be used to monitor disease states, disease progression, drug toxicity, drug efficacy and drug metabolism.

The invention includes methods of diagnosing esophageal cancer in a patient comprising the step of detecting the level of expression in a tissue sample of two or more genes from Tables 2-8; wherein differential expression of the genes in Tables 2-8 is indicative of esophageal cancer. In some preferred embodiments, the method may include detecting the expression level of one or more genes selected from a group consisting of apolipoprotein C-1, galectin 4, keratin 18, annexin A10, cathepsin E, homeobox C10, MPP1, transglutaminase 1, aquaporin 3, trefoil peptide1, trefoil peptide 2 or mucin 5B.

The invention also includes methods of detecting the progression of esophageal cancer. For instance, methods of the invention include detecting the progression of esophageal cancer in a patient comprising the step of detecting the level of expression in a

tissue sample of two or more genes from Tables 2-8; wherein differential expression of the genes in Tables 2-8 is indicative of esophageal cancer progression. In some preferred embodiments, the progression may be the progression of Barrett's esophagus to esophageal cancer. In some preferred embodiments, the method may include detecting the expression
5 level of one or more genes selected from a group consisting of apolipoprotein C-1, galectin 4, keratin 18, annexin A10, cathepsin E, homeobox C10, MPP1, transglutaminase 1, aquaporin 3, trefoil peptide1, trefoil peptide 2 or mucin 5B.

In some aspects, the present invention provides a method of monitoring the treatment of a patient with esophageal cancer, comprising administering a pharmaceutical composition
10 to the patient and preparing a gene expression profile from a cell or tissue sample from the patient and comparing the patient gene expression profile to a gene expression from a cell population comprising normal esophageal cells or to a gene expression profile from a cell population comprising esophageal cancer cells or to both. In some preferred embodiments, the gene profile will include the expression level of one or more genes in Tables 2-8. In other
15 preferred embodiments, one or more genes may be selected from a group consisting of apolipoprotein C-1, galectin 4, keratin 18, annexin A10, cathepsin E, homeobox C10, MPP1, transglutaminase 1, aquaporin 3, trefoil peptide1, trefoil peptide 2 or mucin 5B.

In another aspect, the present invention provides a method of treating a patient with esophageal cancer, comprising administering to the patient a pharmaceutical composition,
20 wherein the composition alters the expression of at least one gene in Tables 2-8, preparing a gene expression profile from a cell or tissue sample from the patient comprising tumor cells and comparing the patient expression profile to a gene expression profile from an untreated cell population comprising esophageal cancer cells.

In one aspect, the present invention provides a method of diagnosing esophageal
25 adenocarcinoma in a patient, comprising detecting the level of expression in a tissue sample of two or more genes from Tables 2-8, wherein differential expression of the genes in Tables 2-8 is indicative of esophageal adenocarcinoma.

In another aspect, the present invention provides a method of detecting the progression of esophageal adenocarcinoma in a patient, comprising detecting the level of
30 expression in a tissue sample of two or more genes from Tables 2-8; wherein differential expression of the genes in Tables 2-8 is indicative of esophageal adenocarcinoma progression.

The present invention also provides materials and methods for monitoring the treatment of a patient with a esophageal adenocarcinoma. The present invention provides a method of monitoring the treatment of a patient with esophageal adenocarcinoma, comprising administering a pharmaceutical composition to the patient, preparing a gene expression
5 profile from a cell or tissue sample from the patient and comparing the patient gene expression profile to a gene expression from a cell population comprising normal esophageal cells or to a gene expression profile from a cell population comprising esophageal adenocarcinoma cells or to both. In some preferred embodiments, the method may include detecting the level of expression of one or more genes selected from a group consisting of
10 apolipoprotein C-1, galectin 4, keratin 18, annexin A10, cathepsin E, homeobox C10, MPP1, transglutaminase 1, aquaporin 3, trefoil peptide1, trefoil peptide 2 or mucin 5B.

In a related aspect, the present invention provides a method of treating a patient with esophageal adenocarcinoma, comprising administering to the patient a pharmaceutical composition, wherein the composition alters the expression of at least one gene in Tables 2-8,
15 preparing a gene expression profile from a cell or tissue sample from the patient comprising esophageal adenocarcinoma cells and comparing the patient expression profile to a gene expression profile from an untreated cell population comprising esophageal adenocarcinoma cells. In some preferred embodiments, one or more genes may be selected from a group consisting of apolipoprotein C-1, galectin 4, keratin 18, annexin A10, cathepsin E,
20 homeobox C10, MPP1, transglutaminase 1, aquaporin 3, trefoil peptide1, trefoil peptide 2 or mucin 5B.

The invention further includes methods of screening for an agent capable of modulating the onset or progression of esophageal cancer, comprising the steps of exposing a cell to the agent; and detecting the expression level of two or more genes from Tables 2-8. In
25 some embodiments, the esophageal cancer may be an esophageal adenocarcinoma. In some preferred embodiments, one or more genes may be selected from a group consisting of apolipoprotein C-1, galectin 4, keratin 18, annexin A10, cathepsin E, homeobox C10, MPP1, transglutaminase 1, aquaporin 3, trefoil peptide1, trefoil peptide 2 or mucin 5B. Preferred methods may detect all or nearly all of the genes in the tables.

30 The invention further includes compositions comprising at least two oligonucleotides, wherein each of the oligonucleotides comprises a sequence that specifically hybridizes to a gene in Tables 2-8 as well as solid supports comprising at least two probes, wherein each of

the probes comprises a sequence that specifically hybridizes to a gene in Tables 2-8. In some preferred embodiments, one or more genes may be selected from a group consisting of apolipoprotein C-1, galectin 4, keratin 18, annexin A10, cathepsin E, homeobox C10, MPP1, transglutaminase 1, aquaporin 3, trefoil peptide1, trefoil peptide 2 or mucin 5B.

5 The invention further includes computer systems comprising a database containing information identifying the expression level in esophageal tissue of a set of genes comprising at least two genes in Tables 2-8 and a user interface to view the information. In some preferred embodiments, one or more genes may be selected from a group consisting of apolipoprotein C-1, galectin 4, keratin 18, annexin A10, cathepsin E, homeobox C10,
10 MPP1, transglutaminase 1, aquaporin 3, trefoil peptide1, trefoil peptide 2 or mucin 5B. The database may further include sequence information for the genes, information identifying the expression level for the set of genes in normal esophageal tissue and cancerous tissue and may contain links to external databases such as GenBank.

Lastly, the invention includes methods of using the databases, such as methods of
15 using the disclosed computer systems to present information identifying the expression level in a tissue or cell of at least one gene in Tables 2-8, comprising the step of comparing the expression level of at least one gene in Tables 2-8 in the tissue or cell to the level of expression of the gene in the database. In some preferred embodiments, one or more genes may be selected from a group consisting of apolipoprotein C-1, galectin 4, keratin 18,
20 annexin A10, cathepsin E, homeobox C10, MPP1, transglutaminase 1, aquaporin 3, trefoil peptide1, trefoil peptide 2 or mucin 5B.

BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 shows the results of a cluster analysis. Figure 1a shows genes under
25 expressed in BA while Figures 1b, 1c and 1d show genes overexpressed in BA.

Figure 2 shows the results of a cluster analysis. Figure 2a shows genes identified as markers for squamous epithelial cells. Figure 2b shows genes involved in extracellular matrix (ECM) modification. Figure 2c shows genes involved in cell adhesion, migration, proliferation and differentiation.

DETAILED DESCRIPTION

Many biological functions are accomplished by altering the expression of various genes through transcriptional (*e.g.*, through control of initiation, provision of RNA precursors, RNA processing, etc.) and/or translational control. For example, fundamental biological processes such as cell cycle, cell differentiation and cell death, are often characterized by the variations in the expression levels of groups of genes.

Changes in gene expression also are associated with pathogenesis. For example, the lack of sufficient expression of functional tumor suppressor genes and/or the over expression of oncogene/protooncogenes could lead to tumorigenesis or hyperplastic growth of cells (Marshall, (1991) *Cell*, 64, 313-326; Weinberg, (1991) *Science*, 254, 1138-1146). Thus, changes in the expression levels of particular genes (*e.g.*, oncogenes or tumor suppressors) serve as signposts for the presence and progression of various diseases.

Monitoring changes in gene expression may also provide certain advantages during drug screening development. Often drugs are screened and prescreened for the ability to interact with a major target without regard to other effects the drugs have on cells. Often such other effects cause toxicity in the whole animal, which prevent the development and use of the potential drug.

Applicants have examined tissue from normal esophageal tissue and tissue from esophageal tumors to identify global changes in gene expression between tumor biopsies and normal tissue. These global changes in gene expression, also referred to as expression profiles, provide useful markers for diagnostic uses as well as markers that can be used to monitor disease states, disease progression, drug toxicity, drug efficacy and drug metabolism.

Expression profiles of genes in particular tissues, disease states or disease progression stages provide molecular tools for evaluating toxicity, drug efficacy, drug metabolism, development, and disease monitoring. Changes in the expression profile from a baseline profile can be used as an indication of such effects. Those skilled in the art can use any of a variety of known techniques to evaluate the expression of one or more of the genes and/or ESTs identified in the instant application in order to observe changes in the expression profile.

The present application has identified differences in gene expression between normal esophageal tissue and esophageal adenocarcinoma. Barrett's epithelium was identified adjacent to many of the cancers. In some cases, the tumor involved an extensive area of

esophageal mucosa suggesting that it had overgrown the Barrett's epithelium from which it derived. Genes and ESTs have been found whose expression significantly varies (>3 fold change up or down) between normal and malignant tissue. In preferred embodiments, the expression level of one or more of these genes and/or ESTs can be determined using as
5 interrogators probes specific to one or more of these genes and/or ESTs. This permits the determination of the expression pattern in unknown cells or samples and their identification as benign or malignant. The expression patterns of the genes and ESTs which were examined are listed in Tables 2-8. The complete sequences of the genes and ESTs are available from GenBank using the Accession numbers shown in each table.

Definitions

In the description that follows, numerous terms and phrases known to those skilled in the art are used. In the interest of clarity and consistency of interpretation, the definitions of certain terms and phrases are provided.

15 The present invention provides compositions and methods to detect the level of expression of genes that may be differentially expressed dependent upon the state of the cell, *i.e.*, normal versus cancerous. As used herein, the phrase "detecting the level expression" includes methods that quantify expression levels as well as methods that determine whether a gene of interest is expressed at all. Thus, an assay which provides a yes or no result without
20 necessarily providing quantification of an amount of expression is an assay that requires "detecting the level of expression" as that phrase is used herein.

As used herein, oligonucleotide sequences that are complementary to one or more of the genes described herein, refers to oligonucleotides that are capable of hybridizing under stringent conditions to at least part of the nucleotide sequence of said genes. Such
25 hybridizable oligonucleotides will typically exhibit at least about 75% sequence identity at the nucleotide level to said genes, preferably about 80% or 85% sequence identity or more preferably about 90% or 95% or more sequence identity to said genes.

"Bind(s) substantially" refers to complementary hybridization between a probe nucleic acid and a target nucleic acid and embraces minor mismatches that can be
30 accommodated by reducing the stringency of the hybridization media to achieve the desired detection of the target polynucleotide sequence.

The terms "background" or "background signal intensity" refer to hybridization signals resulting from non-specific binding, or other interactions, between the labeled target nucleic acids and components of the oligonucleotide array (*e.g.*, the oligonucleotide probes, control probes, the array substrate, etc.). Background signals may also be produced by intrinsic fluorescence of the array components themselves. A single background signal can be calculated for the entire array, or a different background signal may be calculated for each target nucleic acid. In a preferred embodiment, background is calculated as the average hybridization signal intensity for the lowest 5% to 10% of the probes in the array, or, where a different background signal is calculated for each target gene, for the lowest 5% to 10% of the probes for each gene. Of course, one of skill in the art will appreciate that where the probes to a particular gene hybridize well and thus appear to be specifically binding to a target sequence, they should not be used in a background signal calculation. Alternatively, background may be calculated as the average hybridization signal intensity produced by hybridization to probes that are not complementary to any sequence found in the sample (*e.g.*, probes directed to nucleic acids of the opposite sense or to genes not found in the sample such as bacterial genes where the sample is mammalian nucleic acids). Background can also be calculated as the average signal intensity produced by regions of the array that lack any probes at all.

The phrase "hybridizing specifically to" refers to the binding, duplexing or hybridizing of a molecule substantially to or only to a particular nucleotide sequence or sequences under stringent conditions when that sequence is present in a complex mixture (*e.g.*, total cellular) DNA or RNA.

Assays and methods of the invention may utilize available formats to simultaneously screen at least about 100, preferably about 1000, more preferably about 10,000 and most preferably about 1,000,000 or more different nucleic acid hybridizations.

The terms "mismatch control" or "mismatch probe" refer to a probe whose sequence is deliberately selected not to be perfectly complementary to a particular target sequence. For each mismatch (MM) control in a high-density array there typically exists a corresponding perfect match (PM) probe that is perfectly complementary to the same particular target sequence. The mismatch may comprise one or more bases.

While the mismatch(s) may be located anywhere in the mismatch probe, terminal mismatches are less desirable as a terminal mismatch is less likely to prevent hybridization of

the target sequence. In a particularly preferred embodiment, the mismatch is located at or near the center of the probe such that the mismatch is most likely to destabilize the duplex with the target sequence under the test hybridization conditions.

The term "perfect match probe" refers to a probe that has a sequence that is perfectly complementary to a particular target sequence. The test probe is typically perfectly complementary to a portion (subsequence) of the target sequence. The perfect match (PM) probe can be a "test probe", a "normalization control" probe, an expression level control probe and the like. A perfect match control or perfect match probe is, however, distinguished from a "mismatch control" or "mismatch probe."

As used herein a "probe" is defined as a nucleic acid, preferably an oligonucleotide, capable of binding to a target nucleic acid of complementary sequence through one or more types of chemical bonds, usually through complementary base pairing, usually through hydrogen bond formation. As used herein, a probe may include natural (i.e., A, G, U, C or T) or modified bases (7-deazaguanosine, inosine, etc.). In addition, the bases in probes may be joined by a linkage other than a phosphodiester bond, so long as it does not interfere with hybridization. Thus, probes may be peptide nucleic acids in which the constituent bases are joined by peptide bonds rather than phosphodiester linkages.

The term "stringent conditions" refers to conditions under which a probe will hybridize to its target subsequence, but with only insubstantial hybridization to other sequences or to other sequences such that the difference may be identified. Stringent conditions are sequence-dependent and will be different in different circumstances. Longer sequences hybridize specifically at higher temperatures. Generally, stringent conditions are selected to be about 5°C lower than the thermal melting point (T_m) for the specific sequence at a defined ionic strength and pH.

Typically, stringent conditions will be those in which the salt concentration is at least about 0.01 to 1.0 M sodium ion concentration (or other salts) at pH 7.0 to 8.3 and the temperature is at least about 30°C for short probes (e.g., 10 to 50 nucleotide). Stringent conditions may also be achieved with the addition of destabilizing agents such as formamide.

The "percentage of sequence identity" or "sequence identity" is determined by comparing two optimally aligned sequences or subsequences over a comparison window or span, wherein the portion of the polynucleotide sequence in the comparison window may optionally comprise additions or deletions (i.e., gaps) as compared to the reference sequence

(which does not comprise additions or deletions) for optimal alignment of the two sequences. The percentage is calculated by determining the number of positions at which the identical subunit (*e.g.*, nucleic acid base or amino acid residue) occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the window of comparison and multiplying the result by 100 to yield the percentage of sequence identity. Percentage sequence identity when calculated using the programs GAP or BESTFIT (see below) is calculated using default gap weights.

Homology or identity may be determined by **BLAST** (Basic Local Alignment Search Tool) analysis using the algorithm employed by the programs **blastp**, **blastn**, **blastx**, **tblastn** and **tblastx** (Karin *et al.*, (1990) Proc. Natl. Acad. Sci. USA 87, 2264-2268 and Altschul, (1993) J. Mol. Evol. 36, 290-300, fully incorporated by reference) which are tailored for sequence similarity searching. The approach used by the **BLAST** program is to first consider similar segments between a query sequence and a database sequence, then to evaluate the statistical significance of all matches that are identified and finally to summarize only those matches which satisfy a preselected threshold of significance. For a discussion of basic issues in similarity searching of sequence databases, see Altschul *et al.*, ((1994) Nature Genet. 6, 119-129) which is fully incorporated by reference. The search parameters for **histogram**, **descriptions**, **alignments**, **expect** (*i.e.*, the statistical significance threshold for reporting matches against database sequences), **cutoff**, **matrix** and **filter** are at the default settings. The default scoring matrix used by **blastp**, **blastx**, **tblastn**, and **tblastx** is the **BLOSUM62** matrix (Henikoff *et al.*, (1992) Proc. Natl. Acad. Sci. USA 89, 10915-10919, fully incorporated by reference). Four **blastn** parameters were adjusted as follows: Q=10 (gap creation penalty); R=10 (gap extension penalty); wink=1 (generates word hits at every winkth position along the query); and gapw=16 (sets the window width within which gapped alignments are generated). The equivalent **Blastp** parameter settings were Q=9; R=2; wink=1; and gapw=32. A **Bestfit** comparison between sequences, available in the GCG package version 10.0, uses DNA parameters GAP=50 (gap creation penalty) and LEN=3 (gap extension penalty) and the equivalent settings in protein comparisons are GAP=8 and LEN=2.

30 *Uses of Differentially Expressed Genes*

The present invention identifies those genes differentially expressed between normal esophageal tissue and cancerous esophageal tissue. One of skill in the art can select one or

more of the genes identified as being differentially expressed and use the information and methods provided herein to interrogate or test a particular sample. For a particular interrogation of two conditions or sources, it is desirable to select those genes that display a great difference in the expression pattern between the two conditions or sources. At least a two-fold difference is desirable, but a three, five-fold or ten-fold difference may be preferred. Interrogations of the genes or proteins can be performed to yield information on gene expression as well as on the levels of the encoded proteins.

Diagnostic Uses for the Esophageal Cancer Markers

As described herein, the genes and gene expression information provided in Tables 2-8 may be used as diagnostic markers for the prediction or identification of the malignant state of the esophageal tissue. For instance, an esophageal tissue sample or other sample from a patient may be assayed by any of the methods known to those skilled in the art, and the expression levels from one or more genes from Tables 2-8, may be compared to the expression levels found in normal esophageal tissue, tissue from esophageal adenocarcinoma or both. Expression profiles generated from the tissue or other sample that substantially resemble an expression profile from normal or diseased esophageal tissue may be used, for instance, to aid in disease diagnosis. Comparison of the expression data, as well as available sequence or other information may be done by researcher or diagnostician or may be done with the aid of a computer and databases as described herein.

Use of the Esophageal Cancer Markers for Monitoring Disease Progression

Molecular expression markers for esophageal cancer can be used to confirm the type and progression of the cancer made on the basis of morphological criteria. For example, squamous cell carcinoma could be distinguished from adenocarcinoma based on the level and type of genes expressed in a tissue sample. In some situations, identifications of cell type or source is ambiguous based on classical criteria. In these situations the molecular expression markers of the present invention are useful.

In addition, progression of esophageal squamous cell carcinoma to adenocarcinoma can be monitored by following the expression patterns of the involved genes using the molecular expression markers of the present invention. Perturbed expression can be observed

in the diseased state. Monitoring of the efficacy of certain drug regimens can also be accomplished by following the expression patterns of the molecular expression markers.

Although only a few different disease progression time points have been observed, as shown in the examples below, other developmental stages can be studied using these same molecular expression markers. The importance of these markers in development has been shown here, however, variations in their expression may occur at other times. For example, one could study the expression of these markers at benign stages for comparison to expression at malignant states.

As described above, the genes and gene expression information provided in Tables 2-8 may also be used as markers for the monitoring of disease progression, for instance, the development of esophageal cancer. For instance, an esophageal tissue sample or other sample from a patient may be assayed by any of the methods known to those of skill in the art, and the expression levels in the sample from a gene or genes from Tables 2-8 may be compared to the expression levels found in normal esophageal tissue, tissue from esophageal cancer, in particular, Barrett's-associated esophageal adenocarcinoma (BA), or both. Comparison of the expression data, as well as available sequence or other information may be done by researcher or diagnostician or may be done with the aid of a computer and databases as described herein.

Use of the Esophageal Cancer Markers for Drug Screening

Potential drugs can be screened to determine if application of the drug alters the expression of one or more of the genes identified herein. This may be useful, for example, in determining whether a particular drug is effective in treating a particular patient or patient population with esophageal cancer. In the case where the expression of a gene is affected by the potential drug such that its level of expression returns to normal, the drug is indicated in the treatment of esophageal cancer. Similarly, a drug that causes expression of a gene which is not normally expressed by epithelial cells in the esophagus, may be contraindicated in the treatment of esophageal cancer.

According to the present invention, the genes identified in Tables 2-8 may be used as markers to evaluate the effects of a candidate drug or agent on a cell, particularly a cell undergoing malignant transformation, for instance, an esophageal cancer cell or tissue sample. A candidate drug or agent can be screened for the ability to stimulate the transcription or expression of a given marker or markers (drug targets) or to down-regulate or

inhibit the transcription or expression of a marker or markers. According to the present invention, one can also compare the specificity of the effects of a drug by looking at the number of markers affected by the drug and comparing them to the number of markers affected by a different drug. A more specific drug will affect fewer transcriptional targets.

5 Similar sets of markers identified for two drugs indicates a similarity of effects.

Assays to monitor the expression of a marker or markers as defined in Tables 2-8 may utilize any available means of monitoring for changes in the expression level of the nucleic acids of the invention. As used herein, an agent is said to modulate the expression of a nucleic acid of the invention if it is capable of up- or down-regulating expression of the
10 nucleic acid in a cell.

Agents that are assayed in the above methods can be randomly selected or rationally selected or designed. As used herein, an agent is said to be randomly selected when the agent is chosen randomly without considering the specific sequences involved in the association of the a protein of the invention alone or with its associated substrates, binding partners, etc. An
15 example of randomly selected agents is the use a chemical library or a peptide combinatorial library, or a growth broth of an organism.

As used herein, an agent is said to be rationally selected or designed when the agent is chosen on a nonrandom basis which takes into account the sequence of the target site and/or its conformation in connection with the agent's action. Agents can be rationally selected or
20 rationally designed by utilizing the peptide sequences that make up these sites. For example, a rationally selected peptide agent can be a peptide whose amino acid sequence is identical to or a derivative of any functional consensus site.

The agents of the present invention can be, as examples, peptides, small molecules, vitamin derivatives, as well as carbohydrates, lipids, oligonucleotides and covalent and non-
25 covalent combinations thereof. Dominant negative proteins, DNA encoding these proteins, antibodies to these proteins, peptide fragments of these proteins or mimics of these proteins may be introduced into cells to affect function. "Mimic" as used herein refers to the modification of a region or several regions of a peptide molecule to provide a structure chemically different from the parent peptide but topographically and functionally similar to
30 the parent peptide (see Grant, (1995) in Molecular Biology and Biotechnology Meyers (editor) VCH Publishers). A skilled artisan can readily recognize that there is no limit as to the structural nature of the agents of the present invention.

Assay Formats

The genes identified as being differentially expressed in esophageal cancer may be used in a variety of nucleic acid detection assays to detect or quantify the expression level of a gene or multiple genes in a given sample. For example, traditional Northern blotting, nuclease protection, RT-PCR and differential display methods may be used for detecting gene expression levels.

The protein products of the genes identified herein can also be assayed to determine the amount of expression. Methods for assaying for a protein include Western blot, immunoprecipitation, radioimmunoassay. It is preferred, however, that the mRNA be assayed as an indication of expression. Methods for assaying for mRNA include Northern blots, slot blots, dot blots, and hybridization to an ordered array of oligonucleotides. Any method for specifically and quantitatively measuring a specific protein or mRNA or DNA product can be used. However, methods and assays of the invention are most efficiently designed with array or chip hybridization-based methods for detecting the expression of a large number of genes.

Any hybridization assay format may be used, including solution-based and solid support-based assay formats. A preferred solid support is a high density array also known as a DNA chip or a gene chip. In one assay format, gene chips containing probes to at least two genes from Tables 2-8 may be used to directly monitor or detect changes in gene expression in the treated or exposed cell as described herein.

Additional assay formats may be used to monitor the ability of the agent to modulate the expression of a gene identified in Tables 2-8. For instance, as described above, mRNA expression may be monitored directly by hybridization of probes to the nucleic acids of the invention. Cell lines are exposed to an agent to be tested under appropriate conditions and time and total RNA or mRNA is isolated by standard procedures such those disclosed in Sambrook *et al.*, (1989) *Molecular Cloning - A Laboratory Manual*, Cold Spring Harbor Laboratory Press). In some embodiments, it may be desirable to amplify one or more of the RNA molecules isolated prior to application of the RNA to the gene chip. Using techniques well known in the art, the RNA may be reverse transcribed and amplified in the form of DNA or may be reverse transcribed into DNA and the DNA used as a template for transcription to generate recombinant RNA (rRNA). Any method that results in the production of a sufficient quantity of nucleic acid to be hybridized effectively to the gene chip may be used.

In another format, cell lines that contain reporter gene fusions between the open reading frame and/or the 3' or 5' regulatory regions of a gene in Tables 2-8 and any assayable fusion partner may be prepared. Numerous assayable fusion partners are known and readily available including the firefly luciferase gene and the gene encoding chloramphenicol acetyltransferase (Alam *et al.*, (1990) Anal. Biochem. 188, 245-254). Cell lines containing the reporter gene fusions are then exposed to the agent to be tested under appropriate conditions and time. Differential expression of the reporter gene between samples exposed to the agent and control samples identifies agents which modulate the expression of the nucleic acid.

10 In another assay format, cells or cell lines are first identified which express one or more of the gene products of the invention physiologically. Cells and/or cell lines so identified would preferably comprise the necessary cellular machinery to ensure that the transcriptional and/or translational apparatus of the cells would faithfully mimic the response of normal or cancerous esophageal tissue to an exogenous agent. Such machinery would
15 likely include appropriate surface transduction mechanisms and/or cytosolic factors. Such cell lines may be, but are not required to be, derived from esophageal tissue. The cells and/or cell lines may then be contacted with an agent and the expression of one or more of the genes of interest may then be assayed. The genes may be assayed at the mRNA level and/or at the protein level.

20 In some embodiments, such cells or cell lines may be transduced or transfected with an expression vehicle (*e.g.*, a plasmid or viral vector) containing an expression construct comprising an operable 5'-promoter containing end of a gene of interest identified in Tables 2-8 fused to one or more nucleic acid sequences encoding one or more antigenic fragments. The construct may comprise all or a portion of the coding sequence of the gene of interest
25 which may be positioned 5'- or 3'- to a sequence encoding an antigenic fragment. The coding sequence of the gene of interest may be translated or un-translated after transcription of the gene fusion. At least one antigenic fragment may be translated. The antigenic fragments are selected so that the fragments are under the transcriptional control of the promoter of the gene of interest and are expressed in a fashion substantially similar to the expression pattern of the gene of interest. The antigenic fragments may be expressed as
30 polypeptides whose molecular weight can be distinguished from the naturally occurring polypeptides. In some embodiments, gene products of the invention may further comprise an

immunologically distinct tag. Such a process is well known in the art (see Sambrook *et al.*, (1989) Molecular Cloning - A Laboratory Manual, Cold Spring Harbor Laboratory Press).

Cells or cell lines transduced or transfected as outlined above are then contacted with agents under appropriate conditions; for example, the agent comprises a pharmaceutically acceptable excipient and is contacted with cells comprised in an aqueous physiological buffer such as phosphate buffered saline (PBS) at physiological pH, Eagles balanced salt solution (BSS) at physiological pH, PBS or BSS comprising serum or conditioned media comprising PBS or BSS and serum incubated at 37°C. Said conditions may be modulated as deemed necessary by one of skill in the art. Subsequent to contacting the cells with the agent, said cells will be disrupted and the polypeptides of the lysate are fractionated such that a polypeptide fraction is pooled and contacted with an antibody to be further processed by immunological assay (*e.g.*, ELISA, immunoprecipitation or Western blot). The pool of proteins isolated from the "agent-contacted" sample will be compared with a control sample where only the excipient is contacted with the cells and an increase or decrease in the immunologically generated signal from the "agent-contacted" sample compared to the control will be used to distinguish the effectiveness of the agent.

Another embodiment of the present invention provides methods for identifying agents that modulate the levels, concentration or at least one activity of a protein(s) encoded by the genes in Tables 2-8. Such methods or assays may utilize any means of monitoring or detecting the desired activity.

In one format, the relative amounts of a protein of the invention produced in a cell population that has been exposed to the agent to be tested may be compared to the amount produced in an un-exposed control cell population. In this format, probes such as specific antibodies are used to monitor the differential expression of the protein in the different cell populations. Cell lines or populations are exposed to the agent to be tested under appropriate conditions and time. Cellular lysates may be prepared from the exposed cell line or population and a control, unexposed cell line or population. The cellular lysates are then analyzed with the probe, such as a specific antibody.

The genes and ESTs of the present invention may be assayed in any convenient form. For example, they may be assayed in the form mRNA or reverse transcribed mRNA. The genes may be cloned or not and the genes may be amplified or not. The cloning itself does not appear to bias the representation of genes within a population. However, it may be

preferable to use polyA+ RNA as a source, as it can be used with less processing steps. In some embodiments, it may be preferable to assay the protein or peptide encoded by the gene.

The sequences of the expression marker genes are in the public databases. Tables 2-8 provide the Accession numbers and name for each of the sequences. In Tables 2-6, the number following the notation gb= is the GenBank accession number. The sequences of the genes in GenBank are expressly incorporated by reference and are publicly available at, for example, www.ncbi.nih.gov. IMAGE gives the clone number from the IMAGE consortium.

Probe design

Probes based on the sequences of the genes described herein may be prepared by any commonly available method. Oligonucleotide probes for assaying the tissue or cell sample are preferably of sufficient length to specifically hybridize only to appropriate, complementary genes or transcripts. Typically the oligonucleotide probes will be at least 10, 12, 14, 16, 18, 20 or 25 nucleotides in length. In some cases longer probes of at least 30, 40, or 50 nucleotides will be desirable.

One of skill in the art will appreciate that an enormous number of array designs are suitable for the practice of this invention. The high density array will typically include a number of probes that specifically hybridize to the sequences of interest. See WO 99/32660 for methods of producing probes for a given gene or genes. In addition, in a preferred embodiment, the array will include one or more control probes.

High density array chips of the invention include "test probes." Test probes may be oligonucleotides that range from about 5 to about 500 or about 5 to about 50 nucleotides, more preferably from about 10 to about 40 nucleotides and most preferably from about 15 to about 40 nucleotides in length. In other particularly preferred embodiments, the probes are about 20 or 25 nucleotides in length. In another preferred embodiment, test probes are double or single strand DNA sequences. DNA sequences may be isolated or cloned from natural sources or amplified from natural sources using natural nucleic acid as templates. These probes have sequences complementary to particular subsequences of the genes whose expression they are designed to detect. Thus, the test probes are capable of specifically hybridizing to the target nucleic acid they are to detect.

In addition to test probes that bind the target nucleic acid(s) of interest, the high density array can contain a number of control probes. The control probes fall into three

categories referred to herein as (1) normalization controls; (2) expression level controls; and (3) mismatch controls.

5 Normalization controls are oligonucleotide or other nucleic acid probes that are complementary to labeled reference oligonucleotides or other nucleic acid sequences that are added to the nucleic acid sample. The signals obtained from the normalization controls after hybridization provide a control for variations in hybridization conditions, label intensity, "reading" efficiency and other factors that may cause the signal of a perfect hybridization to vary between arrays. In a preferred embodiment, signals (e.g., fluorescence intensity) read from all other probes in the array are divided by the signal (, fluorescence intensity) from the control probes thereby normalizing the measurements.

10 Virtually any probe may serve as a normalization control. However, it is recognized that hybridization efficiency varies with base composition and probe length. Preferred normalization probes are selected to reflect the average length of the other probes present in the array, however, they can be selected to cover a range of lengths. The normalization control(s) can also be selected to reflect the (average) base composition of the other probes in the array, however in a preferred embodiment, only one or a few probes are used and they are selected such that they hybridize well (i.e., no secondary structure) and do not match any target-specific probes.

20 Expression level controls are probes that hybridize specifically with constitutively expressed genes in the biological sample. Virtually any constitutively expressed gene provides a suitable target for expression level controls. Typical expression level control probes have sequences complementary to subsequences of constitutively expressed "housekeeping genes" including, but not limited to the β -actin gene, the transferrin receptor gene, the GAPDH gene, and the like.

25 Mismatch controls may also be provided for the probes to the target genes, for expression level controls or for normalization controls. Mismatch controls are oligonucleotide probes or other nucleic acid probes identical to their corresponding test or control probes except for the presence of one or more mismatched bases. A mismatched base is a base selected so that it is not complementary to the corresponding base in the target sequence to which the probe would otherwise specifically hybridize. One or more mismatches are selected such that under appropriate hybridization conditions (e.g., stringent conditions) the test or control probe would be expected to hybridize with its target sequence,

but the mismatch probe would not hybridize (or would hybridize to a significantly lesser extent). Preferred mismatch probes contain a central mismatch. Thus, for example, where a probe is a twenty-mer, a corresponding mismatch probe may have the identical sequence except for a single base mismatch (*e.g.*, substituting a G, a C or a T for an A) at any of
5 positions 6 through 14 (the central mismatch).

Mismatch probes thus provide a control for non-specific binding or cross hybridization to a nucleic acid in the sample other than the target to which the probe is directed. Mismatch probes also indicate whether a hybridization is specific or not. For example, if the target is present the perfect match probes should be consistently brighter than
10 the mismatch probes. In addition, if all central mismatches are present, the mismatch probes can be used to detect a mutation. The difference in intensity between the perfect match and the mismatch probe ($I_{(PM)} - I_{(MM)}$) provides a good measure of the concentration of the hybridized material.

15 *Nucleic Acid Samples*

As is apparent to one of ordinary skill in the art, nucleic acid samples used in the methods and assays of the invention may be prepared by any available method or process. Methods of isolating total mRNA are also well known to those of skill in the art. For example, methods of isolation and purification of nucleic acids are described in detail in
20 Chapter 3 of *Laboratory Techniques in Biochemistry and Molecular Biology: Hybridization With Nucleic Acid Probes, Part I Theory and Nucleic Acid Preparation*, Tijssen, (1993) (editor) Elsevier Press. Such samples include RNA samples, but also include cDNA synthesized from a mRNA sample isolated from a cell or tissue of interest. Such samples also include DNA amplified from the cDNA, and an RNA transcribed from the amplified
25 DNA. One of skill in the art would appreciate that it may be desirable to inhibit or destroy RNase present in homogenates before homogenates can be used.

Biological samples may be of any biological tissue or fluid or cells from any organism as well as cells raised *in vitro*, such as cell lines and tissue culture cells. Frequently the sample will be a "clinical sample" which is a sample derived from a patient. Typical clinical
30 samples include, but are not limited to, sputum, blood, blood-cells (*e.g.*, white cells), tissue or fine needle biopsy samples, urine, peritoneal fluid, and pleural fluid, or cells therefrom.

Biological samples may also include sections of tissues, such as frozen sections or formalin fixed sections taken for histological purposes.

Solid Supports

5 Solid supports containing oligonucleotide probes for differentially expressed genes can be any solid or semisolid support material known to those skilled in the art. Suitable examples include, but are not limited to, membranes, filters, tissue culture dishes, polyvinyl chloride dishes, beads, test strips, silicon or glass based chips and the like. Suitable glass wafers and hybridization methods are widely available, for example, those disclosed by
10 Beattie (WO 95/11755). Any solid surface to which oligonucleotides can be bound, either directly or indirectly, either covalently or non-covalently, can be used. In some embodiments, it may be desirable to attach some oligonucleotides covalently and others non-covalently to the same solid support.

A preferred solid support is a high density array or DNA chip. These contain a
15 particular oligonucleotide probe in a predetermined location on the array. Each predetermined location may contain more than one molecule of the probe, but each molecule within the predetermined location has an identical sequence. Such predetermined locations are termed features. There may be, for example, from 2, 10, 100, 1000 to 10,000, 100,000 or 400,000 of such features on a single solid support. The solid support, or the area within
20 which the probes are attached may be on the order of a square centimeter.

Oligonucleotide probe arrays for expression monitoring can be made and used according to any techniques known in the art (see for example, Lockhart *et al.*, Nat. Biotechnol. (1996) 14, 1675-1680; McGall *et al.*, Proc. Nat. Acad. Sci. USA (1996) 93, 13555-13460). Such probe arrays may contain at least two or more oligonucleotides that are
25 complementary to or hybridize to two or more of the genes described herein. Such arrays may also contain oligonucleotides that are complementary or hybridize to at least 3, 4, 5, 6, 7, 8, 9, 10, 20, 30, 50, 70 or more the genes described herein.

Oligonucleotide arrays are particularly useful for creating gene expression profiles comparing cancer tissue to adjacent normal tissue.

30 The use of available oligonucleotide arrays enabled the determination of the expression levels of numerous genes and ESTs simultaneously. From this mass of

expression data, differentially expressed genes were identified using Fold Change and Gene Signature Differential analysis.

Gene Signature Differential analysis is a method designed to detect genes present in one sample set, and absent in another. Genes with differential expression in cancer tissue
5 versus normal tissue are better diagnostic and therapeutic targets than genes that do not change in expression.

Methods of forming high density arrays of oligonucleotides with a minimal number of synthetic steps are known. The oligonucleotide analogue array can be synthesized on a solid substrate by a variety of methods, including, but not limited to, light-directed chemical
10 coupling, and mechanically directed coupling (see Pirrung *et al.*, (1992) U.S. Patent No. 5,143, 854; Fodor *et al.*, (1998) U.S. Patent No. 5,800,992; Chee *et al.*, (1998) 5,837,832

In brief, the light-directed combinatorial synthesis of oligonucleotide arrays on a glass surface proceeds using automated phosphoramidite chemistry and chip masking techniques. In one specific implementation, a glass surface is derivatized with a silane reagent containing
15 a functional group, *e.g.*, a hydroxyl or amine group blocked by a photolabile protecting group. Photolysis through a photolithographic mask is used selectively to expose functional groups which are then ready to react with incoming 5' photoprotected nucleoside phosphoramidites. The phosphoramidites react only with those sites which are illuminated (and thus exposed by removal of the photolabile blocking group). Thus, the
20 phosphoramidites only add to those areas selectively exposed from the preceding step. These steps are repeated until the desired array of sequences have been synthesized on the solid surface. Combinatorial synthesis of different oligonucleotide analogues at different locations on the array is determined by the pattern of illumination during synthesis and the order of addition of coupling reagents.

25 In addition to the foregoing, additional methods which can be used to generate an array of oligonucleotides on a single substrate are described in Fodor *et al.*, (1993). WO 93/09668. High density nucleic acid arrays can also be fabricated by depositing premade or natural nucleic acids in predetermined positions. Synthesized or natural nucleic acids are deposited on specific locations of a substrate by light directed targeting and oligonucleotide
30 directed targeting. Another embodiment uses a dispenser that moves from region to region to deposit nucleic acids in specific spots.

Hybridization

Nucleic acid hybridization simply involves contacting a probe and target nucleic acid under conditions where the probe and its complementary target can form stable hybrid duplexes through complementary base pairing (see Lockhart *et al.*, (1999) WO 99/32660).

- 5 The nucleic acids that do not form hybrid duplexes are then washed away leaving the hybridized nucleic acids to be detected, typically through detection of an attached detectable label. It is generally recognized that nucleic acids are denatured by increasing the temperature or decreasing the salt concentration of the buffer containing the nucleic acids. Under low stringency conditions (*e.g.*, low temperature and/or high salt) hybrid duplexes
- 10 (*e.g.*, DNA-DNA, RNA-RNA or RNA-DNA) will form even where the annealed sequences are not perfectly complementary. Thus, specificity of hybridization is reduced at lower stringency. Conversely, at higher stringency (*e.g.*, higher temperature or lower salt) successful hybridization requires fewer mismatches. One of skill in the art will appreciate that hybridization conditions may be selected to provide any degree of stringency. In a
- 15 preferred embodiment, hybridization is performed at low stringency, in this case in 6× SSPE-T at 37°C (0.005% Triton x-100) to ensure hybridization and then subsequent washes are performed at higher stringency (*e.g.*, 1× SSPE-T at 37°C) to eliminate mismatched hybrid duplexes. Successive washes may be performed at increasingly higher stringency (*e.g.*, down to as low as 0.25× SSPE-T at 37°C to 50°C until a desired level of hybridization specificity is
- 20 obtained. Stringency can also be increased by addition of agents such as formamide. Hybridization specificity may be evaluated by comparison of hybridization to the test probes with hybridization to the various controls that can be present (*e.g.*, expression level control, normalization control, mismatch controls, etc.).

- In general, there is a tradeoff between hybridization specificity (stringency) and signal
- 25 intensity. Thus, in a preferred embodiment, the wash is performed at the highest stringency that produces consistent results and that provides a signal intensity greater than approximately 10% of the background intensity. Thus, in a preferred embodiment, the hybridized array may be washed at successively higher stringency solutions and read between each wash. Analysis of the data sets thus produced will reveal a wash stringency above which the hybridization
- 30 pattern is not appreciably altered and which provides adequate signal for the particular oligonucleotide probes of interest.

Signal Detection

The hybridized nucleic acids are typically detected by detecting one or more labels attached to the sample nucleic acids. The labels may be incorporated by any of a number of means well known to those of skill in the art (see Lockhart *et al.*, (1999) WO 99/32660).

5

Databases

The present invention includes relational databases containing sequence information, for instance for the genes of Tables 2-8, as well as gene expression information in various esophageal tissue samples. Databases may also contain information associated with a given
10 sequence or tissue sample such as descriptive information about the gene associated with the sequence information, or descriptive information concerning the clinical status of the tissue sample, or the patient from which the sample was derived. The database may be designed to include different parts, for instance a sequences database and a gene expression database. Methods for the configuration and construction of such databases are widely available, for
15 instance, see Akerblom *et al.*, (1999) U.S. Patent 5,953,727, which is specifically incorporated herein by reference in its entirety.

The databases of the invention may be linked to an outside or external database. In a preferred embodiment, as described in Tables 2-8, the external database is GenBank and the associated databases maintained by the National Center for Biotechnology Information
20 (NCBI).

Any appropriate computer platform may be used to perform the necessary comparisons between sequence information, gene expression information and any other information in the database or provided as an input. For example, a large number of computer workstations are available from a variety of manufacturers, such as those available
25 from Silicon Graphics. Client-server environments, database servers and networks are also widely available and appropriate platforms for the databases of the invention.

The databases of the invention may be used to produce, among other things, electronic Northern blots to allow the user to determine the cell type or tissue in which a given gene is expressed and to allow determination of the abundance or expression level of a given gene in
30 a particular tissue or cell.

The databases of the invention may also be used to present information identifying the expression level in a tissue or cell of a set of genes comprising at least one gene in Tables 2-8

comprising the step of comparing the expression level of at least one gene in Tables 2-8 in the tissue to the level of expression of the gene in the database. Such methods may be used to predict the physiological state of a given tissue by comparing the level of expression of a gene or genes in Tables 2-8 from a sample to the expression levels found in tissue from normal esophageal tissue, tissue from esophageal adenocarcinoma or both. Such methods may also be used in the drug or agent screening assays as described herein.

Without further description, it is believed that one of ordinary skill in the art can, using the preceding description and the following illustrative examples, make and utilize the compounds of the present invention and practice the claimed methods. The following working examples therefore, specifically point out the preferred embodiments of the present invention, and are not to be construed as limiting in any way the remainder of the disclosure.

EXAMPLES

Example 1: Tissue Sample Acquisition and Preparation

For tissue specimens, nine normal esophagus samples and eight BA tissue samples, which included seven matched tumor-normal sets, were used. Six of the eight BA samples were lymph node invasive.

With minor modifications, the sample preparation protocol followed the Affymetrix GeneChip Expression Analysis Manual. Frozen tissue was first ground to powder using the Spex Certiprep 6800 Freezer Mill. Total RNA was then extracted using Trizol (Life Technologies). The total RNA yield for each sample (average tissue weight of 300 mg) was 200-500 μ g. Next, mRNA was isolated using the Oligotex mRNA Midi kit (Qiagen). Since the mRNA was eluted in a final volume of 400 μ l, an ethanol precipitation step was required to bring the concentration to 1 μ g/ μ l. Using 1-5 μ g of mRNA, double stranded cDNA was created using the SuperScript Choice system (Gibco-BRL). First strand cDNA synthesis was primed with a T7-(dT₂₄) oligonucleotide. The cDNA was then phenol-chloroform extracted and ethanol precipitated to a final concentration of 1 μ g/ μ l.

From 2 μ g of cDNA, cRNA was synthesized according to standard procedures. To biotin label the cRNA, nucleotides Bio-11-CTP and Bio-16-UTP (Enzo Diagnostics) were added to the reaction. After a 37°C incubation for six hours, the labeled cRNA was cleaned up according to the RNeasy Mini kit protocol (Qiagen). The cRNA was then fragmented (5×

fragmentation buffer: 200 mM Tris-Acetate (pH 8.1), 500 mM KOAc, 150 mM MgOAc) for thirty-five minutes at 94°C.

55 µg of fragmented cRNA was hybridized on the human and the Human Genome U95 set of arrays for twenty-four hours at 60 rpm in a 45°C hybridization oven. The chips were washed and stained with Streptavidin Phycoerythrin (SAPE) (Molecular Probes) in Affymetrix fluidics stations. To amplify staining, SAPE solution was added twice with an anti-streptavidin biotinylated antibody (Vector Laboratories) staining step in between. Hybridization to the probe arrays was detected by fluorometric scanning (Hewlett Packard Gene Array Scanner). Following hybridization and scanning, the microarray images were analyzed for quality control, looking for major chip defects or abnormalities in hybridization signal. After all chips passed QC, the data was analyzed using Affymetrix GeneChip software (v3.0), and Experimental Data Mining Tool (EDMT) software (v1.0).

Example 2: Gene Expression Analysis

15 All samples were prepared as described and hybridized onto the Affymetrix Human Genome U95 array set.

Each chip contains 16-20 oligonucleotide probe pairs per gene or cDNA clone. These probe pairs include perfectly matched sets and mismatched sets, both of which are necessary for the calculation of the average difference. The average difference is a measure of the intensity difference for each probe pair, calculated by subtracting the intensity of the mismatch from the intensity of the perfect match. This takes into consideration variability in hybridization among probe pairs and other hybridization artifacts that could affect the fluorescence intensities. Using the average difference value that has been calculated, the GeneChip software then makes an absolute call for each gene or EST.

25 The absolute call of present, absent or marginal is used to generate a Gene Signature, a tool used to identify those genes that are commonly present or commonly absent in a given sample set, according to the absolute call. For each set of samples, a median average difference was figured using the average differences of each individual sample within the set. The Gene Signature for one set of samples is compared to the Gene Signature of another set of samples to determine the Gene Signature Differential. This comparison identifies the genes that are consistently present in one set of samples and consistently absent in the second set of samples.

The Gene Signature Curve is a graphic view of the number of genes consistently present in a given set of samples as the sample size increases, taking into account the genes commonly expressed among a particular set of samples, and discounting those genes whose expression is variable among those samples. The curve is also indicative of the number of samples necessary to generate an accurate Gene Signature. As the sample number increases, the number of genes common to the sample set decreases. The curve is generated using the positive Gene Signatures of the samples in question, determined by adding one sample at a time to the Gene Signature, beginning with the sample with the smallest number of present genes and adding samples in ascending order. The curve displays the sample size required for the most consistency and the least amount of expression variability from sample to sample. The point where this curve begins to level off represents the minimum number of samples required for the Gene Signature. Graphed on the x-axis is the number of samples in the set, and on the y-axis is the number of genes in the positive Gene Signature. As a general rule, the acceptable percent of variability in the number of positive genes between two sample sets should be less than 5%.

Example 3: Expression Profiles

Using the above described methods, genes that were predominantly over-expressed in BA, or predominantly under-expressed in BA were identified. The revealed genes were used to identify gene clusters generated by hierarchical clustering that exhibited a consistent fold change and/or dominant expression pattern between the normal and diseased sample sets. Genes with consistent differential expression patterns provide potential targets for broad range diagnostics and therapeutics.

First, the expression profiles of the nine normal esophagus samples were pooled and used to determine the genes that are commonly expressed or commonly not expressed. To find the expression pattern consistent to disease, the same procedure was followed with the eight samples from patients with BA. Table 1 lists, by array type, the number of genes with expression patterns common to the majority of normal or diseased samples.

Next, the unique pattern of genes over-expressed in the disease was identified by determining those genes that were commonly expressed in BA, but commonly NOT expressed in normal esophagus. Similarly, the unique pattern of genes under-expressed in disease was found by identifying genes that were expressed in the majority of normal

esophagus samples, but NOT expressed in the majority of BA samples. Table 1 lists the number of genes uniquely under-expressed and over-expressed in BA by array type. With this method 423 genes were identified to be unique for BA.

5 Example 4: Fold Change analysis

The data was first filtered to exclude all genes that showed no expression in any of the samples. The ratio (tumor/normal) was calculated by comparing the mean expression value for each gene in the BA sample set against the mean expression value of that gene in the normal esophagus sample set. Genes were included in the analysis if they had a fold change ≥ 3 in either direction, and a P value < 0.05 as determined by a two-tail unequal variance t-test. Out of the ~60,000 genes surveyed by the Human Genome U95 set, 1584 genes were present in the overall fold change analysis, 701 were over-expressed in BA and 883 were under-expressed in BA. Out of the 423 unique genes for BA (244 under-expressed and 179 over-expressed) previously identified, 170 were also present in the fold change analysis.

15 Determining these 170 genes independently by both methods overcomes the limitations of accuracy inherent in either method. These 170 key disease-related genes have both significant overall fold changes, and 87 are not detectable in BA while the remaining 83 are not detectable in normal esophagus.

The genes identified in the fold change analysis are listed in Tables 2-6. Table 2 lists those genes identified using the Human Genome U95A chip, Table 3 lists those genes identified using the Human Genome U95B chip, Table 4 lists those genes identified using the Human Genome U95C chip, Table 5 lists those genes identified using the Human Genome U95D chip and Table 6 lists those genes identified using the Human Genome U95E chip.

25 Example 5: Cluster Analysis

The data was first filtered to exclude all genes that showed no expression in any of the samples. To normalize the data, fold change values for the samples were calculated by dividing each gene expression value by the mean of the expression values for all samples, both normal esophagus and BA, for that gene. Genes were included in the cluster analysis if they had at least one instance of a fold change ≥ 3 in either direction, and a P value of < 0.05 as assessed by a two-tail unequal variance t-test. Using a hierarchical clustering algorithm, genes were grouped according to their expression pattern similarities across all samples

(Eisen, *et al.*, Cluster analysis and display of genome-wide expression patterns. *Proc. Natl. Acad. Sci. USA* **95**, 14863-14868 (1998)).

For the Human Genome U95A array, 1100 full-length known genes or ESTs (8.7% of the genes present on the array) were included in the cluster analysis. The resulting dendrogram (Fig. 1) grouped all nine normal esophagus samples and seven of the eight BA samples into separate trees. BA sample 316 clustered in a branch with its matched normal esophagus sample (315) rather than with the other tumors. A number of genes on the Human Genome U95A array are present in duplicate. In most cases the duplicate genes cluster next to each other or in close proximity of each other, verifying internal microarray reproducibility. Four clusters were chosen for in-depth analyses, based on the presence of a portion of the 170 key disease-related genes previously identified by our fingerprinting and fold change analysis methods. Figure 1 shows the results obtained using a hierarchical clustering to measure expression variation for 1100 full-length genes present on the Affymetrix Human Genome U95A oligonucleotide array. Four clusters (a-d) are presented that include genes from the 170 gene list identified by both our analysis methods. Those genes are labeled in red. Cluster (a) contains genes under-expressed in Barrett's-associated esophageal adenocarcinoma (BA), while clusters (b-d) contain genes over-expressed in BA. The dendrogram summarizes the expression similarities between samples. Each gene is represented by a single row, and each sample by a single column. Relative to the mean expression level of all samples, red squares represent an over-expression, green squares represent an under-expression, black squares represent no expression change, and grey squares denote a missing sample. The overall fold change (FC), the fold change calculated between the two groups of samples, for each gene is also listed.

Figure 2 shows the results obtained from a clustering analysis performed for 4,521 genes from the Human Genome U95 array set. A representative cluster was chosen that contained a number of genes from the U95A (Figure 1 cluster d). Genes in common between clusters are labeled in green. Based on expression similarities to known genes, the biological function of ESTs can be determined. The genes thus identified are listed in Table 8.

The cluster analysis also identified genes not identified in the fold change analysis. Table 7 provides a list of those genes identified as present in the U95A chip cluster analysis but not identified as present in the fold change analysis.

The clusters of genes thus identified contain genes that exhibit a consistent fold change between the normal and diseased sample sets, providing targets for broad range diagnostics and therapeutics.

5 **Example 6: Tissue markers**

As the progression from normal esophagus to BA occurs, squamous epithelial cells are replaced with a heterogeneous population of columnar cells that exhibit both intestinal and gastric-like characteristics. The methods of the present invention were used to identify clusters containing genes differentially expressed in all normal or diseased samples. The
10 genes thus identified were screened for the presence of marker genes corresponding to gross morphological changes.

The stratified squamous epithelial terminal differentiation markers, transglutaminase 1, transglutaminase 3, involucrin, envoplakin, periplakin and sciellin were all present in the cluster of genes under-expressed in BA (Figure 1a). A distinct cluster (Figure 1c) was also
15 identified that included over-expressed genes associated with the Barrett's esophagus phenotype (see Labouvie, *et al.*, Differential expression of mucins and trefoil peptides in native epithelium, Barrett's metaplasia and squamous cell carcinoma of the oesophagus. *J. Cancer Res. Clin. Oncol.* 125, 71-6 (1999) and Westerveld, *et al.*, Gastric proteases in Barrett's esophagus. *Gastroenterology* 93, 774-8 (1987)). The genes trefoil peptide 1 (TFF-
20 1), trefoil peptide 2 (TFF-2), mucin 5B, and pepsinogen C were present in this cluster.

Example 7: Metastasis-related genes

The majority of BA tumors in this study (6 out of 8) displayed regional lymph node invasion. Genes with expression changes that correlate highly with the metastatic phenotype
25 are very valuable diagnostic markers. The first step in metastasis is the loss of cell adhesion at the primary site. Desmosomes are multi-component structures involved in epithelial cell to cell adhesion and intracellular anchoring of intermediate filaments. The desmosomal components, desmoglein 3, desmocollin 2, and desmoplakin, are all present in the cluster of genes under-expressed in BA (Figure 1a).

30 Once cell to cell adhesion is broken, the extracellular matrix (ECM) must be breached to enable movement into metastatic sites. A number of proteases, including metalloproteinase 1 (MMP-1), metalloproteinase 11 (MMP-11), cathepsin E, cathepsin K,

and urokinase plasminogen activator (u-PA), that are involved in basement membrane and ECM degradation are spread throughout the clusters containing genes over-expressed in BA (Figures 1b-1d). MMP-1, MMP-11, and u-PA expression has previously been correlated with metastasis and /or poor prognosis in esophageal carcinoma (see Murray, *et al.*, Matrix metalloproteinase-1 is associated with poor prognosis in oesophageal cancer. *J. Pathol.* **185**, 256-61 (1998), Porte, *et al.*, Overexpression of stromelysin-3, BM-40/SPARC, and MET genes in human esophageal carcinoma: implications for prognosis. *Clin. Cancer Res.* **4**, 1375-82 (1998) and Hewin, *et al.*, Plasminogen activators in oesophageal carcinoma. *Br. J. Surg.* **83**, 1152-5 (1996)).

In parallel with the expression increase in ECM proteinases, an expression decrease was seen in a number of proteinase inhibitors, including squamous cell carcinoma antigen 1 (SCCA1), squamous cell carcinoma antigen 2 (SCCA2), cystatin 6, and ELANH2 (Fig. 3A, i). The loss of inhibitory proteinases may allow metastatic tumor progression to occur more rapidly.

As the tumor moves through the stromal compartment into secondary sites, a balance must be reached between ECM degradation and renewal. The tumor requires the break down of ECM components to enable invasion, but the stromal environment must also be altered to create an environment with which the tumor can adhere and migrate. SPARC/osteonectin, SPP1/osteopontin, and thrombospondin-2 are secreted proteins involved in mediating cell to matrix interactions. These genes cluster together (Figure 1d), and are over-expressed in BA. SPARC, SPP-1, and thrombospondin-1 have previously been linked to oesophageal carcinoma (see Porte, *et al.*, *supra*, Casson, *et al.*, Ras mutation and expression of the ras-regulated genes osteopontin and cathepsin L in human esophageal cancer. *Int. J. Cancer* **72**, 739-45 (1997) and Oshiba, *et al.*, Stromal thrombospondin-1 expression is correlated with progression of esophageal squamous cell carcinoma. *Anticancer Res.* **19**, 4375-8 (1999)).

Further denoting the changes in the stromal environment, the ECM components, chondroitin sulfate proteoglycan 2, collagen type XI alpha 1, and collagen type X alpha 1, are also present in this cluster (Figure 1d).

Example 8: Other Gene Clusters

A number of additional clusters, besides those directly related to the metastatic process, have been identified. Reflecting a change in the tumor's transcriptional program,

one distinct cluster under-expressed in BA contained the homeobox genes, PITX1, PAX9 and BARX2 (Figure 1a). The homeobox gene, HOXB7, was over-expressed in BA (Figure 1b). Homeobox genes are nuclear transcription factors that regulate development. Another cluster contained genes elicited by the body's anti-tumoral immune response (Figure 1b). Two genes induced by interferon alpha and beta, IFI35 and IFI30, two genes induced by interferon gamma, ISG15 and GIP3, and interferon-induced complement component C2 were present in a cluster over-expressed in BA (Figure 1b). Natural killer transcript 4 (NK4) also clusters with these genes.

10 **Example 9: EST Clustering**

Clustering was performed for the full Human Genome U95 set. After filtering, 4521 genes (7.5% of the genes present on all 5 arrays) were analyzed via hierarchical clustering and the results are shown in Figure 2. A list of the genes thus identified is provided in Table 8. A hierarchical clustering was used to measure expression variation for 4,521 known genes or ESTs from the Affymetrix HG-U95 array set. Three clusters are shown that include genes from the HG-U95A analysis (see Figure 1). Genes in common between clusters are labeled in green. The dendrogram summarizes expression similarities between samples. Each gene and sample presentation is the same as in Figure 1. The overall fold change (FC), fold change between the groups of tissue samples, are also listed for each gene. Based on expression similarities to known genes, the biological function of some EST's can be assigned. Cluster A represents a number of marker genes for squamous epithelial cells. ESTs grouped around these genes are novel diagnostic markers whose expression loss follows BA progression. Cluster B represents a number of genes involved in ECM modification. Cluster C represents genes involved in cell adhesion, migration, proliferation and differentiation. Interestingly, EST AA877900 clusters around the cell surface protein encoded by tetraspanins and shows homology to the mouse cell surface antigen 114/A10 precursor. The resulting dendrogram grouped all nine normal oesophagus and all eight BA samples into separate trees. Figure 2 shows the incorporation of these additional genes, consisting primarily of ESTs, into the Human Genome U95A cluster (Figure 1). The U95A cluster contained a number of proteins involved in extracellular matrix modification and structure. Based on expression similarities to known genes, the biological function of surrounding ESTs can be postulated. Supporting this theory, the extracellular matrix

proteins, collagen type V alpha 2, biglycan, and SPP1 (osteopontin) are represented in the new cluster (Figure 2).

The present invention provides methods to identify genes and ESTs that are differentially expressed in normal and cancerous esophageal tissue. The method entails using
5 several tissues of the same disease type to identify the gene expression patterns that are unique to normal and diseased tissues, comparing these patterns to determine the expression patterns that uniquely identify the disease, and performing fold change analysis to discover which genes are the most important determinants of disease. Applying the method, Applicants have identified key disease-related genes, and furthermore demonstrate that these
10 weighted genes, can be used to identify significant clusters generated by hierarchical clustering algorithms. This overall approach, can potentially determine novel targets for diagnostic and therapeutic intervention in a wide variety of tissues, as demonstrated here with BA.

Although the present invention has been described in detail with reference to
15 examples above, it is understood that various modifications can be made without departing from the spirit of the invention. Accordingly, the invention is limited only by the following claims. All cited patents and publications referred to in this application are herein incorporated by reference in their entirety.

Table 1. A) Affymetrix probe array data was used to determine the number of genes expressed in normal esophagus and the number of genes NOT expressed in Barrett's-associated esophageal adenocarcinoma (BA). Relative to gene expression in normal esophagus, 244 genes were uniquely under-expressed in BA. B) The number of genes expressed in BA was compared against the number of normal esophagus genes whose expression was NOT detectable. 179 genes were uniquely over-expressed in BA.

	HG-U95A	HG-U95B	HG-U95C	HG-U95D	HG-U95E	Totals
A)						
No. of genes whose expression was detected in normal esophagus	5652	4394	2743	699	1266	14754
No. of genes whose expression was not detected in BA	5123	6158	8162	10397	8017	37857
No. of genes uniquely under-expressed in BA	101	62	46	20	15	244
B)						
No. of genes whose expression was detected in BA	5433	4659	2772	934	1667	15465
No. of genes whose expression was not detected in normal esophagus	4170	5347	7184	9621	8163	34485
No. of genes uniquely over-expressed in BA	47	51	19	25	37	179
Sum of genes unique for BA						423

Table 2. U95_A Fold Change Genes (>3 over-expressed in Barrett's associated esophageal adenocarcinoma (BA), <0.33 under-expressed in BA)

Affy ID	Gene Name	Fold Change	P-value
38469_at	Cluster Incl M35252:Human CO-029 /cds=(137,850) /gb=M35252 /gi=180925 /ug=Hs.84072 /len=1083	33.86361231	0.000002
38582_at	Cluster Incl A1961220:wt15b04.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2507503 /clone_end=3" /gb=A1961220 /gi=5753933 /ug=Hs.181286 /len=510"	30.1318728	0.000014
765_s_at	AB006781 /FEATURE= /DEFINITION=AB006781 Homo sapiens mRNA for galectin-4, complete cds	20.91494437	0.000002
608_at	M12529 /FEATURE=mRNA /DEFINITION=HUMAPOE Human apolipoprotein E mRNA, complete cds	16.55132436	0
31798_at	Cluster Incl AA314825:EST186646 Homo sapiens cDNA, 5 end /clone=ATCC-111986 /clone_end=5" /gb=AA314825 /gi=1967154 /ug=Hs.1406 /len=574"	13.40389513	0.003038
37186_s_	Cluster Incl U11863:Human clone HP-DAO2 diamine oxidase, copper/topa quinone containing mRNA, complete cds /cds=(73,2385) /gb=U11863 /gi=533537 /ug=Hs.75741 /len=2473	12.17002487	0.000007
38827_at	Cluster Incl AF038451:Homo sapiens secreted cement gland protein XAG-2 homolog (hAG-2(R) mRNA, complete cds /cds=(58,585) /gb=AF038451 /gi=3779225 /ug=Hs.91011 /len=1059	11.64190393	0.000049
33327_at	Cluster Incl AB023171:Homo sapiens mRNA for KIAA0954 protein, partial cds /cds=(0,2682) /gb=AB023171 /gi=4589551 /ug=Hs.184640 /len=5057	10.57914803	0.000175
38239_at	Cluster Incl A1312905:qp84d03.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1929701 /clone_end=3" /gb=A1312905 /gi=4018510 /ug=Hs.16762 /len=493"	10.52282698	0.004857
41106_at	Cluster Incl AF022797:Homo sapiens intermediate conductance calcium-activated potassium channel (hKCa4) mRNA, complete cds /cds=(396,1679) /gb=AF022797 /gi=2674355 /ug=Hs.10082 /len=2238	9.590462962	0.005712
34342_s_	Cluster Incl AF052124:Homo sapiens clone 23810 osteopontin mRNA, complete cds /cds=(87,989) /gb=AF052124 /gi=3360431 /ug=Hs.313 /len=1504	9.533960576	0.000045
575_s_at	M93036 /FEATURE=mRNA /DEFINITION=HUMGA7A08 Human (clone 21726) carcinoma-associated antigen GA733-2 (GA733-2) mRNA, exon 9 and complete cds	8.991837359	0.000002
35832_at	Cluster Incl AB029000:Homo sapiens mRNA for KIAA1077 protein, partial cds /cds=(0,2456) /gb=AB029000 /gi=5689490 /ug=Hs.70823 /len=4834	8.290812823	0.000042

Table 2. U95_A Fold Change Genes (>3 over-expressed in Barrett's associated esophageal adenocarcinoma (BA), <0.33 under-expressed in BA)

Affy ID	Gene Name	Fold Change	P-value
32349_at	Cluster Incl AJ238979: Homo sapiens mRNA for annexin A10 protein (ANXA10 gene) /cds=(117,1091) /gb=AJ238979 /gi=5689749 /ug=Hs.188401 /len=1408	8.241398197	0.004318
271_s_at	J05036 /FEATURE=mRNA /DEFINITION=HUMCTSE Human cathepsin E mRNA, complete cds	8.235638183	0.000008
39945_at	Cluster Incl U09278: Human fibroblast activation protein mRNA, complete cds /cds=(208,2490) /gb=U09278 /gi=1888315 /ug=Hs.418 /len=2814	7.883016283	0.000057
1890_at	AB000584 /FEATURE= /DEFINITION=AB000584 Homo sapiens mRNA for TGF-beta superfamily protein, complete cds	7.410761415	0.000062
37319_at	Cluster Incl M35878: Human insulin-like growth factor-binding protein-3 gene, complete cds, clone HL1006d /cds=(132,1007) /gb=M35878 /gi=184522 /ug=Hs.77326 /len=3446	7.315749117	0.00202
38124_at	Cluster Incl X55110: Human mRNA for neurite outgrowth-promoting protein /cds=(25,456) /gb=X55110 /gi=35086 /ug=Hs.82045 /len=786	7.314122689	0.0002
36781_at	Cluster Incl X01683: Human mRNA for alpha 1-antitrypsin /cds=(38,1294) /gb=X01683 /gi=28965 /ug=Hs.75621 /len=1371	7.157108509	0.000155
38428_at	Cluster Incl M13509: Human skin collagenase mRNA, complete cds /cds=(68,1477) /gb=M13509 /gi=180664 /ug=Hs.83169 /len=1970	6.752025797	0.000234
33699_at	Cluster Incl M18667: Human pepsinogen C gene /cds=(73,1230) /gb=M18667 /gi=189820 /ug=Hs.1867 /len=1359	6.70507087	0.007673
41470_at	Cluster Incl AF027208: Homo sapiens AC133 antigen mRNA, complete cds /cds=(37,2634) /gb=AF027208 /gi=2688948 /ug=Hs.112360 /len=3794	6.236624008	0.000202
1107_s_at	M13755 /FEATURE=mRNA /DEFINITION=HUMIFN15K Human interferon-induced 17-kDa/15-kDa protein mRNA, complete cds	6.024908182	0.000042
33702_f.a	Cluster Incl L05144: Homo sapiens (clone lamda-hPEC-3) phosphoenolpyruvate carboxykinase (PCK1) mRNA, complete cds /cds=(121,1989) /gb=L05144 /gi=189944 /ug=Hs.1872 /len=2657	5.944698576	0.000527
38261_at	Cluster Incl AF085692: Homo sapiens multidrug resistance-associated protein 3B (MRP3) mRNA, complete cds /cds=(36,1568) /gb=AF085692 /gi=4106443 /ug=Hs.90786 /len=5327	5.920947513	0.001318
40079_at	Cluster Incl AA156240: z150c12.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-505366 /clone_end=3" /gb=AA156240 /gi=1727858 /ug=Hs.154737 /len=668"	5.897828308	0.000012
41585_at	Cluster Incl AB018289: Homo sapiens mRNA for KIAA0746 protein, partial cds /cds=(0,3091) /gb=AB018289 /gi=3882212 /ug=Hs.49500 /len=4086	5.679597385	0.00001

Table 2. U95_A Fold Change Genes (>3 over-expressed in Barrett's associated esophageal adenocarcinoma (BA), <0.33 under-expressed in BA)

Affy ID	Gene Name	Fold Change	P-value
40201_at	Cluster Incl M76180:Human aromatic amino acid decarboxylase (ddc) mRNA, complete cds /cds=(69,1511) /gb=M76180 /gi=181520 /ug=Hs.150403 /len=1930	5.655152421	0.00268
39395_at	Cluster Incl AA704137:ag47g01.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1119984 /clone_end=3" /gb=AA704137 /gi=2714055 /ug=Hs.125359 /len=923"	5.386956374	0.0002
2092_s_at	J04765 /FEATURE= /DEFINITION=HUMOSTRO Human osteopontin mRNA, complete cds	5.386687312	0.008537
39119_s_	Cluster Incl AA631972:fmfc39 Homo sapiens cDNA /clone=CR7-5 /gb=AA631972 /gi=2554583 /ug=Hs.943 /len=896	5.364323204	0.000015
34775_at	Cluster Incl AF065388:Homo sapiens tetraspan NET-1 mRNA, complete cds /cds=(121,846) /gb=AF065388 /gi=3152700 /ug=Hs.38972 /len=1278	5.286352347	0.000004
38181_at	Cluster Incl X57766:Human stromelysin-3 mRNA /cds=(9,1475) /gb=X57766 /gi=456256 /ug=Hs.155324 /len=2247	5.282204273	0.001357
38615_at	Cluster Incl AF097021:Homo sapiens GW112 protein (GW112) mRNA, complete cds /cds=(508,1071) /gb=AF097021 /gi=3860076 /ug=Hs.100347 /len=2830	5.282142721	0.01537
33731_at	Cluster Incl AJ130718:Homo sapiens mRNA for glycoprotein-associated amino acid transporter y+LAT1 /cds=(293,1828) /gb=AJ130718 /gi=3970724 /ug=Hs.194693 /len=2214	5.179186526	0.001054
37117_at	Cluster Incl Z83838:Human DNA sequence from PAC 127B20 on chromosome 22q11.2-qter, contains gene for GTPase-activating protein similar to rhoGAP protein. ribosomal protein L6 pseudogene, ESTs and CA repeat /cds=(0,926) /gb=Z83838 /gi=2276307 /ug=Hs.102336 /len=927	5.160630589	0.006643
39339_at	Cluster Incl AB018335:Homo sapiens mRNA for KIAA0792 protein, complete cds /cds=(250,2673) /gb=AB018335 /gi=3882304 /ug=Hs.119387 /len=4074	5.158180582	0.000121
41764_at	Cluster Incl AA976838:oa35c12.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1588342 /clone_end=3" /gb=AA976838 /gi=3154284 /ug=Hs.182778 /len=468"	5.012716912	0.002917
1451_s_at	D13666 /FEATURE= /DEFINITION=HUMOSF2OS Homo sapiens osf-2 mRNA for osteoblast specific factor 2 (OSF-2os), complete cds	4.951150996	0.000646
36883_at	Cluster Incl X14640:Human mRNA for keratin 13 /cds=(42,1418) /gb=X14640 /gi=34032 /ug=Hs.74070 /len=1691	4.916594286	0.000477
35703_at	Cluster Incl X06374:Human mRNA for platelet-derived growth factor PDGF-A /cds=(403,993) /gb=X06374 /gi=35363 /ug=Hs.37040 /len=2305	4.875862208	0.003643

Table 2. U95_A Fold Change Genes (>3 over-expressed in Barrett's associated esophageal adenocarcinoma (BA), <0.33 under-expressed in BA)

Affy ID	Gene Name	Fold Change	P-value
1358_s_at	U22970/FEATURE=mRNA#1 /DEFINITION=HSU22970 Human interferon-inducible peptide (6-16) gene, complete cds	4.830291781	0.000138
35822_at	Cluster Incl L15702:Human complement factor B mRNA, complete cds /cds=(40,2334) /gb=L15702 /gi=291921 /ug=Hs.69771 /len=2388	4.749292589	0.0006
38432_at	Cluster Incl AA203213:zx57e04.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-446622 /clone_end=5" /gb=AA203213 /gi=1798923 /ug=Hs.833 /len=879	4.746919578	0.00033
40462_at	Cluster Incl AF055022:Homo sapiens clone 24684 mRNA sequence /cds=UNKNOWN /gb=AF055022 /gi=3005750 /ug=Hs.168073 /len=1864	4.654507719	0.002269
35313_at	Cluster Incl AB002308:Human mRNA for KIAA0310 gene, complete cds /cds=(1655,4300) /gb=AB002308 /gi=2224560 /ug=Hs.5716 /len=5955	4.633034993	0.000025
40762_g	Cluster Incl AA705628:zf40a01.s1 Homo sapiens cDNA, 3 end /clone=379368 /clone_end=3" /gb=AA705628 /gi=2715546 /ug=Hs.90911 /len=514	4.598316089	0.005112
32306_g	Cluster Incl J03464:Human collagen alpha-2 type I mRNA, complete cds, clone pHCOL2A1 /cds=(469,4569) /gb=J03464 /gi=179595 /ug=Hs.179573 /len=5416	4.574917305	0.000593
31901_at	Cluster Incl AF044253:Homo sapiens potassium channel beta 2 subunit (HKvbeta2.2) mRNA, alternatively spliced, complete cds /cds=(0,1061) /gb=AF044253 /gi=2827465 /ug=Hs.154417 /len=1062	4.485703929	0.000413
35766_at	Cluster Incl M26326:Human keratin 18 mRNA, complete cds /cds=(51,1343) /gb=M26326 /gi=186690 /ug=Hs.65114 /len=1412	4.434133847	0.000464
36495_at	Cluster Incl U21931:Human fructose-1,6-biphosphatase (FBP1) gene /cds=(211,1227) /gb=U21931 /gi=1000077 /ug=Hs.574 /len=1476	4.359840196	0.000517
33118_at	Cluster Incl U73167:Homo sapiens cosmid clone LUCA14 from 3p21.3 /cds=(0,2252) /gb=U73167 /gi=2880032 /ug=Hs.82222 /len=2253	4.325421706	0.001122
38111_at	Cluster Incl X15998:H.sapiens mRNA for the chondroitin sulphate proteoglycan versican, V1 splice-variant; precursor peptide /cds=(266,7495) /gb=X15998 /gi=37662 /ug=Hs.81800 /len=8224	4.314531945	0.005225
34712_at	Cluster Incl AB023227:Homo sapiens mRNA for KIAA1010 protein, partial cds /cds=(0,3949) /gb=AB023227 /gi=4589669 /ug=Hs.23860 /len=5524	4.249345789	0.006337
36482_s	Cluster Incl Y15724:Homo sapiens SERCA3 gene, exons 1-7 (and joined CDS) /cds=(152,3241) /gb=Y15724 /gi=3021395 /ug=Hs.5541 /len=4800	4.242412448	0.000245

Table 2. U95_A Fold Change Genes (>3 over-expressed in Barrett's associated esophageal adenocarcinoma (BA), <0.33 under-expressed in BA)

Affy ID	Gene Name	Fold Change	P-value
39801_at	Cluster Incl AF046889:Homo sapiens lysyl hydroxylase isoform 3 (PLOD3) mRNA, complete cds /cds=(216,2432) /gb=AF046889 /gi=3153234 /ug=Hs.153357 /len=2735	4.237391894	0.001831
39959_at	Cluster Incl AL031983:dJ271M21.6 (Diubiquitin) /cds=(18,515) /gb=AL031983 /gi=4160199 /ug=Hs.44532 /len=777	4.224484244	0.013448
38671_at	Cluster Incl AB014520:Homo sapiens mRNA for KIAA0620 protein, partial cds /cds=(0,5957) /gb=AB014520 /gi=3327053 /ug=Hs.105958 /len=6754	4.204467196	0.000003
34022_at	Cluster Incl M36821:Human cytokine (GRO-gamma) mRNA, complete cds /cds=(77,397) /gb=M36821 /gi=183632 /ug=Hs.89690 /len=1064	4.186691813	0.003842
33904_at	Cluster Incl AB000714:Homo sapiens hRVP1 mRNA for RVP1, complete cds /cds=(198,860) /gb=AB000714 /gi=2570128 /ug=Hs.25640 /len=1250	4.160312065	0.009967
1930_at	U83659 /FEATURE= /DEFINITION=HSU83659 Human multidrug resistance-associated protein homolog (MRP3) mRNA, partial cds	4.103745262	0.001081
38646_s	Cluster Incl AF763065:wi64h03.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2398133 /clone_end=3" /gb=AF763065 /gi=5178732 /ug=Hs.1032 /len=670"	4.034467285	0.045602
35937_at	Cluster Incl U65416:Human MHC class I molecule (MICB) gene, complete cds /cds=(5,1156) /gb=U65416 /gi=1815636 /ug=Hs.211580 /len=2367	4.031356856	0.004886
36174_at	Cluster Incl X70326:H.sapiens MacMarcks mRNA /cds=(13,600) /gb=X70326 /gi=38434 /ug=Hs.75061 /len=1334	4.021774238	0.006155
34433_at	Cluster Incl AF035299:Homo sapiens clone 23863 mRNA, partial cds /cds=(0,1531) /gb=AF035299 /gi=2661055 /ug=Hs.103854 /len=1953	3.999547716	0.000374
34251_at	Cluster Incl M92299:Human homeobox 2.1 protein (HOX2A) mRNA, complete cds /cds=(275,1084) /gb=M92299 /gi=184292 /ug=Hs.22554 /len=2037	3.989655556	0.002597
1230_g_at	U78556 /FEATURE= /DEFINITION=HSU78556 Human cisplatin resistance associated alpha protein (hCRA alpha) mRNA, complete cds	3.986593947	0.007319
41812_s	Cluster Incl AB020713:Homo sapiens mRNA for KIAA0906 protein, partial cds /cds=(0,2772) /gb=AB020713 /gi=4240300 /ug=Hs.56966 /len=4217	3.955302442	0.001398
33489_at	Cluster Incl U47292:Human spasmodic polypeptide (SP) gene, 5 region and /cds=(0,389) /gb=U47292 /gi=1477544 /ug=Hs.2979 /len=965"	3.951274898	0.000058

Table 2. U95_A Fold Change Genes (>3 over-expressed in Barrett's associated esophageal adenocarcinoma (BA), <0.33 under-expressed in BA)

Affy ID	Gene Name	Fold Change	P-value
40712_at	Cluster Incl D26579: Homo sapiens mRNA for transmembrane protein, complete cds /cds=(9,2483) /gb=D26579 /gi=1864004 /ug=Hs.86947 /len=3236	3.926351461	0.000403
33322_i_a	Cluster Incl X57348: H. sapiens mRNA (clone 9112) /cds=(165,911) /gb=X57348 /gi=23939 /ug=Hs.184510 /len=1407	3.918698039	0.000123
36976_at	Cluster Incl D21255: Human mRNA for OB-cadherin-2, complete cds /cds=(476,2557) /gb=D21255 /gi=575578 /ug=Hs.75929 /len=3867	3.912909005	0.000009
39340_at	Cluster Incl M16424: Human beta-hexosaminidase alpha chain (HEXA) gene /cds=(0,1589) /gb=M16424 /gi=179457 /ug=Hs.119403 /len=1590	3.895118855	0
1586_at	M35878 /FEATURE=expanded_cds /DEFINITION=HUMIBP3 Human insulin-like growth factor-binding protein-3 gene, complete cds, clone HL1006d	3.855842022	0.010079
925_at	J03909 /FEATURE= /DEFINITION=HUMIIP Human gamma-interferon-inducible protein (IP-30) mRNA, complete cds	3.854414845	0.000001
37276_at	Cluster Incl U51903: Human RasGAP-related protein (IQGAP2) mRNA, complete cds /cds=(222,4949) /gb=U51903 /gi=1262925 /ug=Hs.78993 /len=5767	3.836460946	0.004826
37618_at	Cluster Incl M16937: Human homeo box c1 protein, mRNA, complete cds /cds=(99,752) /gb=M16937 /gi=184300 /ug=Hs.819 /len=1359	3.827480523	0.000352
32609_at	Cluster Incl A1885852: w62d08.x1 Homo sapiens cDNA, 3' end /clone=IMAGE-2429487 /clone_end=3" /gb=A1885852 /gi=5591016 /ug=Hs.795 /len=580"	3.790091828	0.000766
40118_at	Cluster Incl X07290: Human HF.12 gene mRNA /cds=(0,589) /gb=X07290 /gi=32072 /ug=Hs.155470 /len=1801	3.770379359	0.000033
2087_s_at	D21254 /FEATURE= /DEFINITION=HUMOSF4A Human mRNA for OB-cadherin-1, complete cds	3.756489413	0.001994
1482_g_at	L23808 /FEATURE= /DEFINITION=HUMHME Human metalloproteinase (HME) mRNA, complete cds	3.724668585	0.001197
182_at	U01062 /FEATURE=mRNA /DEFINITION=HUMIP3R3 Human type 3 inositol 1,4,5-trisphosphate receptor (ITPR3) mRNA, complete cds	3.723090192	0.000948
39542_at	Cluster Incl AF059611: Homo sapiens nuclear matrix protein NRP/B (NRPB) mRNA, complete cds /cds=(399,2168) /gb=AF059611 /gi=3309572 /ug=Hs.104925 /len=4784	3.700905422	0.000005
32072_at	Cluster Incl U40434: Human mesothelin or CAK1 antigen precursor mRNA, complete cds /cds=(99,1985) /gb=U40434 /gi=1145723 /ug=Hs.155981 /len=2114	3.700537751	0.019363

Table 2. U95_A Fold Change Genes (>3 over-expressed in Barrett's associated esophageal adenocarcinoma (BA), <0.33 under-expressed in BA)

Affy ID	Gene Name	Fold Change	P-value
36197_at	Cluster Incl Y08374:H.sapiens gene encoding cartilage GP-39 protein, exon 1 and 2 (and joined CDS) /cds=(126,127) /gb=Y08374 /gi=2121309 /ug=Hs.75184 /len=1925	3.695365733	0.000483
36184_at	Cluster Incl L06419:Homo sapiens lysyl hydroxylase (PLOD) mRNA, complete cds /cds=(200,2383) /gb=L06419 /gi=190073 /ug=Hs.75093 /len=3115	3.684437007	0.000536
35362_at	Cluster Incl AB018342:Homo sapiens mRNA for KIAA0799 protein, partial cds /cds=(0,2138) /gb=AB018342 /gi=3882318 /ug=Hs.61638 /len=5613	3.622214911	0.000505
39649_at	Cluster Incl X78817:H.sapiens partial C1 mRNA /cds=(42,2882) /gb=X78817 /gi=840785 /ug=Hs.3109 /len=3236	3.589352648	0.006513
1693_s_at	D11139 /FEATURE=exons#1-4 /DEFINITION=HUMTIMP Human gene for tissue inhibitor of metalloproteinases, partial sequence	3.581791533	0.001006
38566_at	Cluster Incl X60382:H.sapiens COL10A1 gene for collagen (alpha-1 type X) /cds=(0,2042) /gb=X60382 /gi=30094 /ug=Hs.179729 /len=3198	3.568272096	0.023539
39043_at	Cluster Incl AF006084:Homo sapiens Arp2/3 protein complex subunit p41-Arc (ARC41) mRNA, complete cds /cds=(80,1198) /gb=AF006084 /gi=2282033 /ug=Hs.11538 /len=1408	3.563560014	0.000113
35926_s	Cluster Incl AF004230:Homo sapiens monocyte/macrophage Ig-related receptor MIR-7 (MIR cl-7) mRNA, complete cds /cds=(170,2125) /gb=AF004230 /gi=2343108 /ug=Hs.204040 /len=2882	3.560518932	0.019359
38332_at	Cluster Incl U83993:Human P2X4 purinoreceptor mRNA, complete cds /cds=(309,1475) /gb=U83993 /gi=4099120 /ug=Hs.9610 /len=2031	3.540548694	0.000001
37542_at	Cluster Incl D86961:Human mRNA for KIAA0206 gene, partial cds /cds=(0,581) /gb=D86961 /gi=1503995 /ug=Hs.79299 /len=4249	3.531781728	0.00014
33374_at	Cluster Incl L09708:Human complement component 2 (C2) gene allele b /cds=(271,2529) /gb=L09708 /gi=2804581 /ug=Hs.2253 /len=2844	3.50128085	0.043555
35372_r_a	Cluster Incl M17017:Human beta-thromboglobulin-like protein mRNA, complete cds /cds=(90,389) /gb=M17017 /gi=179579 /ug=Hs.624 /len=1639	3.492697198	0.004805
38464_at	Cluster Incl X87237:H.sapiens mRNA for processing a-glucosidase I /cds=(132,2642) /gb=X87237 /gi=2344809 /ug=Hs.83919 /len=2854	3.488460577	0.000501
33730_at	Cluster Incl AF095448:Homo sapiens putative G protein-coupled receptor (RAIG1) mRNA, complete cds /cds=(99,1172) /gb=AF095448 /gi=4063889 /ug=Hs.194691 /len=2288	3.420612984	0.000001

Table 2. U95_A Fold Change Genes (>3 over-expressed in Barrett's associated esophageal adenocarcinoma (BA), <0.33 under-expressed in BA)

Affy ID	Gene Name	Fold Change	P-value
37310_at	Cluster Incl X02419:H.sapiens uPA gene /cds=(119,1414) /gb=X02419 /gi=37601 /ug=Hs.77274 /len=2344	3.389908873	0.000181
32305_at	Cluster Incl J03464:Human collagen alpha-2 type I mRNA, complete cds, clone pHCOL2A1 /cds=(469,4569) /gb=J03464 /gi=179595 /ug=Hs.179573 /len=5416	3.385860182	0.00189
38388_at	Cluster Incl M11810:Human (2-5'') oligo A synthetase E gene /cds=(0,1202) /gb=M11810 /gi=189323 /ug=Hs.82396 /len=1552	3.354436847	0.00674
37423_at	Cluster Incl U30246:Human bumetanide-sensitive Na-K-Cl cotransporter (NKCC1) mRNA, complete cds /cds=(164,3802) /gb=U30246 /gi=903681 /ug=Hs.110736 /len=4098	3.349808467	0.003674
464_s_at	U72882 /FEATURE= /DEFINITION=HSU72882 Human interferon-induced leucine zipper protein (IFP35) mRNA, partial cds	3.328892723	0.000109
36732_at	Cluster Incl A1004207:ot94g05.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1624472 /clone_end=3" /gb=A1004207 /gi=3213717 /ug=Hs.55879 /len=517	3.3206594	0.004758
32629_f a	Cluster Incl U90552:Human butyrophilin (BTF5) mRNA, complete cds /cds=(359,1900) /gb=U90552 /gi=2062705 /ug=Hs.167740 /len=3416	3.282634677	0.015555
38607_at	Cluster Incl AF027204:Homo sapiens putative tetraspan transmembrane protein L6H (TM4SF5) mRNA, complete cds /cds=(32,625) /gb=AF027204 /gi=2587053 /ug=Hs.184194 /len=708	3.279897454	0.001734
35355_at	Cluster Incl AB020697:Homo sapiens mRNA for KIAA0890 protein, complete cds /cds=(143,3727) /gb=AB020697 /gi=4240268 /ug=Hs.6141 /len=3800	3.279064388	0.00002
39230_at	Cluster Incl AL022318:BK150C2.2 (Phorbolin 3) /cds=(29,1177) /gb=AL022318 /gi=4826439 /ug=Hs.226307 /len=1512	3.24749805	0.000479
33813_at	Cluster Incl A1813532:wj83a09.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2409400 /clone_end=3" /gb=A1813532 /gi=5424738 /ug=Hs.204298 /len=733	3.24556325	0.001423
40333_at	Cluster Incl U43842:Homo sapiens bone morphogenetic protein-4 (hBMP-4) gene, complete cds /cds=(435,1661) /gb=U43842 /gi=3850194 /ug=Hs.68879 /len=1946	3.244861857	0.003231
38064_at	Cluster Incl X79882:H.sapiens lrp mRNA /cds=(105,2795) /gb=X79882 /gi=895839 /ug=Hs.80680 /len=2816	3.242458638	0.000285
36642_at	Cluster Incl J00287:Human pepsinogen gene /cds=(55,1221) /gb=J00287 /gi=189798 /ug=Hs.75558 /len=1381	3.238347007	0.004957

Table 2. U95_A Fold Change Genes (>3 over-expressed in Barrett's associated esophageal adenocarcinoma (BA), <0.33 under-expressed in BA)

Affy ID	Gene Name	Fold Change	P-value
658_at	L12350 /FEATURE=mrna /DEFINITION=HUMTHRPO Human thrombospondin 2 (THBS2) mRNA, complete cds	3.207772873	0.013942
35345_at	Cluster Incl X83618:H.sapiens mRNA for 3-hydroxy-3-methylglutaryl coenzyme A synthase /cds=(51,1577) /gb=X83618 /gi=619876 /ug=Hs.59889 /len=2043	3.189979043	0.000053
36194_at	Cluster Incl M63959:Human alpha-2-macroglobulin receptor-associated protein mRNA, complete cds /cds=(13,1086) /gb=M63959 /gi=177873 /ug=Hs.75140 /len=1493	3.189185993	0.004792
37637_at	Cluster Incl U27655:Human RGP3 mRNA, complete cds /cds=(287,1846) /gb=U27655 /gi=1216368 /ug=Hs.82294 /len=2638	3.161911203	0.001763
37200_at	Cluster Incl J04162:Human leukocyte IgG receptor (Fc-gamma-R) mRNA, complete cds /cds=(17,718) /gb=J04162 /gi=183036 /ug=Hs.763 /len=1977	3.134424959	0.00002
33127_at	Cluster Incl U89942:Human lysyl oxidase-related protein (WS9-14) mRNA, complete cds /cds=(247,2571) /gb=U89942 /gi=1890107 /ug=Hs.83354 /len=3432	3.13386346	0.020488
33890_at	Cluster Incl AB008109:Homo sapiens mRNA for RGS5, complete cds /cds=(81,626) /gb=AB008109 /gi=2554613 /ug=Hs.24950 /len=2076	3.122107461	0.000677
38363_at	Cluster Incl W60864:zd27g05.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-341912 /clone_end=3" /gb=W60864 /gi=1367661 /ug=Hs.9963 /len=541"	3.115921272	0.0026
39167_r a	Cluster Incl D83174:Human mRNA for collagen binding protein 2, complete cds /cds=(87,1343) /gb=D83174 /gi=1199486 /ug=Hs.9930 /len=2047	3.112282703	0.000802
31856_at	Cluster Incl Z24680:H.sapiens gap gene mRNA, complete CDS /cds=(94,2082) /gb=Z24680 /gi=439295 /ug=Hs.151641 /len=4153	3.10615755	0.000566
1717_s_at	U45878 /FEATURE= /DEFINITION=HSU45878 Human inhibitor of apoptosis protein 1 mRNA, complete cds	3.096213742	0.001867
659_g_at	L12350 /FEATURE=mrna /DEFINITION=HUMTHRPO Human thrombospondin 2 (THBS2) mRNA, complete cds	3.089235008	0.007846
753_at	D86425 /FEATURE= /DEFINITION=D86425 Homo sapiens mRNA for osteonidogen, complete cds	3.077550233	0.001355
32193_at	Cluster Incl AF030339:Homo sapiens receptor for viral semaphorin protein (VESPR) mRNA, complete cds /cds=(249,4955) /gb=AF030339 /gi=3176761 /ug=Hs.184697 /len=5121	3.076341896	0.001147
38612_at	Cluster Incl M69023:Human globin gene /cds=UNKNOWN /gb=M69023 /gi=183127 /ug=Hs.100090 /len=1119	3.067377921	0.000648

Table 2. U95_A Fold Change Genes (>3 over-expressed in Barrett's associated esophageal adenocarcinoma (BA), <0.33 under-expressed in BA)

Affy ID	Gene Name	Fold Change	P-value
32634_s_	Cluster Incl U38260:Human islet cell autoantigen ICAp69 mRNA, complete cds /cds=(169,942) /gb=U38260 /gi=1675205 /ug=Hs.167927 /len=1415	3.064088746	0.002374
38311_at	Cluster Incl AF055012: Homo sapiens clone 24615 mRNA sequence /cds=UNKNOWN /gb=AF055012 /gi=3005735 /ug=Hs.94785 /len=1757	3.057506025	0.000007
34871_at	Cluster Incl W30677:zb75h10.r1 Homo sapiens cDNA, 5' end /clone=IMAGE-309475 /clone_end=5" /gb=W30677 /gi=1311730 /ug=Hs.5019 /len=614"	3.046742301	0.00934
32128_at	Cluster Incl Y13710:Homo sapiens mRNA for alternative activated macrophage specific CC chemokine 1 /cds=(70,339) /gb=Y13710 /gi=2326515 /ug=Hs.16530 /len=779	3.044427861	0.001745
39421_at	Cluster Incl D43969:Human AML1 mRNA for AML1c protein (alternatively spliced product), complete cds /cds=(444,1886) /gb=D43969 /gi=966998 /ug=Hs.129914 /len=6212	3.036973884	0.001109
41354_at	Cluster Incl U25997:Homo sapiens stanniocalcin precursor (STC) mRNA, complete cds /cds=(284,1027) /gb=U25997 /gi=3006202 /ug=Hs.25590 /len=3881	3.032061085	0.001245
35064_at	Cluster Incl X81006:H.sapiens HCG I mRNA /cds=UNKNOWN /gb=X81006 /gi=531406 /ug=Hs.104114 /len=1224	3.024314786	0.005685
35127_at	Cluster Incl AI039144:ox31b09.s1 Homo sapiens cDNA, 3' end /clone=IMAGE-1657913 /clone_end=3" /gb=AI039144 /gi=3278338 /ug=Hs.121017 /len=527"	3.011925912	0.024025
31720_s_	Cluster Incl M10905:Human cellular fibronectin mRNA /cds=(0,2383) /gb=M10905 /gi=182696 /ug=Hs.118162 /len=2384	0.329485955	0.002116
32618_at	Cluster Incl X93086:H.sapiens mRNA for biliverdin IX alpha reductase /cds=(60,950) /gb=X93086 /gi=1246748 /ug=Hs.81029 /len=1053	0.329108511	0.00447
36684_at	Cluster Incl M21154:Human S-adenosylmethionine decarboxylase mRNA, complete cds /cds=(248,1252) /gb=M21154 /gi=178517 /ug=Hs.75744 /len=1805	0.328867318	0.001013
32668_at	Cluster Incl AL080076:Homo sapiens mRNA; cDNA DKFZp564C0362 (from clone DKFZp564C0362) /cds=(59,1144) /gb=AL080076 /gi=5262486 /ug=Hs.169833 /len=1711	0.32860867	0.000001
38158_at	Cluster Incl D79987:Human mRNA for KIAA0165 gene, complete cds /cds=(1113,6500) /gb=D79987 /gi=1136391 /ug=Hs.153479 /len=6662	0.328288405	0.000035
31525_s_	Cluster Incl J00153:Human alpha globin gene cluster on chromosome 16- zeta gene /cds=(0,428) /gb=J00153 /gi=183794 /ug=Hs.182374 /len=429	0.328281737	0.008516

Table 2. U95_A Fold Change Genes (>3 over-expressed in Barrett's associated esophageal adenocarcinoma (BA), <0.33 under-expressed in BA)

Affy ID	Gene Name	Fold Change	P-value
38010_at	Cluster Incl AF002697: Homo sapiens E1B 19K/Bcl-2-binding protein Nip3 mRNA, nuclear gene encoding mitochondrial protein, complete cds /cds=(126,710) /gb=AF002697 /gi=2511528 /ug=Hs.79428 /len=1518	0.328241183	0.005897
33559_at	Cluster Incl U61412: Human non-receptor type protein tyrosine kinase (PTK6) gene /cds=(813,2168) /gb=U61412 /gi=3551752 /ug=Hs.51133 /len=3527	0.328077412	0.003401
41320_s_	Cluster Incl U69609: Human transcriptional repressor (GCF2) mRNA, complete cds /cds=(124,2382) /gb=U69609 /gi=3421044 /ug=Hs.239894 /len=3505	0.327287446	0.0018
39120_at	Cluster Incl AA224832: nc33b06.s1 Homo sapiens cDNA /clone=IMAGE-1009907 /gb=AA224832 /gi=1846120 /ug=Hs.94360 /len=447	0.327269934	0.000091
36214_at	Cluster Incl U70663: Human zinc finger transcription factor hEZF (EZF) mRNA, complete cds /cds=(503,1915) /gb=U70663 /gi=1857160 /ug=Hs.236377 /len=1953	0.326147693	0.003789
38508_s_	Cluster Incl U89337: Human HLA class III region containing cAMP response element binding protein-related protein (CREB-RP) and tenascin X (tenascin-X) genes, complete cds /cds=(0,12869) /gb=U89337 /gi=1841544 /ug=Hs.169886 /len=12870	0.325801777	0.03159
41257_at	Cluster Incl D16217: Human mRNA for calpastatin, complete cds /cds=(162,2288) /gb=D16217 /gi=303598 /ug=Hs.226067 /len=2493	0.32559376	0.014175
38407_r_a	Cluster Incl AI207842: ao89h09.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1953089 /clone_end=3" /gb=AI207842 /gi=3769784 /ug=Hs.8272 /len=771"	0.325385636	0.038443
39159_at	Cluster Incl X99656: H.sapiens mRNA for protein containing SH3 domain, SH3GL1 /cds=(15,1121) /gb=X99656 /gi=1869809 /ug=Hs.97616 /len=2349	0.324435334	0.000015
853_at	S74017 /FEATURE= /DEFINITION=S74017 Nrf2=NF-E2-like basic leucine zipper transcriptional activator [human, hemin-induced K562 cells, mRNA, 2304 nt]	0.323486825	0.002917
33839_at	Cluster Incl D26350: Human mRNA for type 2 inositol 1,4,5-trisphosphate receptor, complete cds /cds=(418,8523) /gb=D26350 /gi=450468 /ug=Hs.238272 /len=10524	0.322681628	0.014546
39693_at	Cluster Incl N53547: yv43b12.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-245471 /clone_end=3" /gb=N53547 /gi=1194713 /ug=Hs.13662 /len=665"	0.320728331	0.014542
40508_at	Cluster Incl AF025887: Homo sapiens glutathione S-transferase A4-4 (GSTA4) mRNA, complete cds /cds=(73,741) /gb=AF025887 /gi=3046391 /ug=Hs.169907 /len=1260	0.320203001	0.011333

Table 2. U95_A Fold Change Genes (>3 over-expressed in Barrett's associated esophageal adenocarcinoma (BA), <0.33 under-expressed in BA)

Affy ID	Gene Name	Fold Change	P-value
1590_s_at	J00277 /FEATURE=cds /DEFINITION=HUMRASH Human (genomic clones lambda-[SK2-T2, HS578T]; cDNA clones RS-[3.4, 6]) c-Ha-ras1 proto-oncogene, complete coding sequence	0.319460667	0.001811
351_f_at	D28423 /FEATURE= /DEFINITION=HUMPSF82 Human mRNA for pre-mRNA splicing factor SRp20, 5'UTR (sequence from the 5'cap to the start codon)	0.318411751	0.000636
871_s_at	M95585 /FEATURE=mRNA /DEFINITION=HUMHLF Human hepatic leukemia factor (HLF) mRNA, complete cds	0.317171499	0.001365
33113_at	Cluster Incl U65093:Human msg1-related gene 1 (mrg1) mRNA, complete cds /cds=(199,840) /gb=U65093 /gi=1853998 /ug=Hs.82071 /len=899	0.316986667	0.00001
32380_at	Cluster Incl Z34974:H.sapiens mRNA for plakophilin (partial) /cds=(252,2432) /gb=Z34974 /gi=550114 /ug=Hs.198382 /len=2680	0.316462158	0.01096
863_g_at	U04313 /FEATURE= /DEFINITION=HSU04313 Human maspin mRNA, complete cds	0.316356159	0.000203
32666_at	Cluster Incl U19495:Human intercrine-alpha (hiRH) mRNA, complete cds /cds=(473,742) /gb=U19495 /gi=1754834 /ug=Hs.169672 /len=2244	0.316156704	0.000461
34197_at	Cluster Incl X80907:H.sapiens mRNA for p85 beta subunit of phosphatidylinositol-3-kinase /cds=(241,2427) /gb=X80907 /gi=2160047 /ug=Hs.211586 /len=3201	0.314829826	0.004387
39908_at	Cluster Incl AF069735:Homo sapiens PCAF associated factor 65 alpha mRNA, complete cds /cds=(0,1868) /gb=AF069735 /gi=3335558 /ug=Hs.131846 /len=1869	0.314036765	0.001203
33421_s_	Cluster Incl AB016247:Homo sapiens mRNA for sterol-C5-desaturase, complete cds /cds=(81,980) /gb=AB016247 /gi=3721881 /ug=Hs.227947 /len=2104	0.313717219	0.000009
39669_at	Cluster Incl AJ009985:Homo sapiens mRNA for annexin 31 /cds=(436,1452) /gb=AJ009985 /gi=3688369 /ug=Hs.3346 /len=1762	0.312453495	0.002723
36496_at	Cluster Incl AF014398:Homo sapiens myo-inositol monophosphatase 2 mRNA, complete cds /cds=(141,1007) /gb=AF014398 /gi=2406665 /ug=Hs.5753 /len=1428	0.310618357	0.002251
40684_at	Cluster Incl U78190:Human GTP cyclohydrolase I feedback regulatory protein gene, complete cds /cds=(94,348) /gb=U78190 /gi=1698996 /ug=Hs.83081 /len=712	0.310587584	0.000134
32363_at	Cluster Incl AF059214:Homo sapiens cholesterol 25-hydroxylase mRNA, complete cds /cds=(10,828) /gb=AF059214 /gi=4038307 /ug=Hs.194687 /len=1360	0.30897539	0.000255
39364_s_	Cluster Incl Y18207:Homo sapiens mRNA for protein phosphatase 1 (PPP1R5) /cds=(91,1044) /gb=Y18207 /gi=3805818 /ug=Hs.12112 /len=1158	0.308335729	0.000446

Table 2: U95_A Fold Change Genes (>3 over-expressed in Barrett's associated esophageal adenocarcinoma (BA), <0.33 under-expressed in BA)

Affy ID	Gene Name	Fold Change	P-value
33305_at	Cluster Incl M93056: Human monocyte/neutrophil elastase inhibitor mRNA sequence /cds=UNKNOWN /gb=M93056 /gi=188621 /ug=Hs.183583 /len=1298	0.307283402	0.000768
37662_at	Cluster Incl A1701164: we10g07.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2340732 /clone_end=3" /gb=A1701164 /gi=4989064 /ug=Hs.78563 /len=777"	0.306979084	0.000015
1490_at	M19720 /FEATURE=mRNA#2 /DEFINITION=HUMMYC3L Human L-myc protein gene, complete cds	0.306261149	0.000001
34986_at	Cluster Incl AF030455: Homo sapiens epithelial V-like antigen precursor (EVA) mRNA, complete cds /cds=(119,766) /gb=AF030455 /gi=3169829 /ug=Hs.151602 /len=1342	0.305646698	0
41359_at	Cluster Incl Z98265: Homo sapiens mRNA for plakophilin 3 /cds=(74,2467) /gb=Z98265 /gi=4995640 /ug=Hs.26557 /len=2808	0.304122892	0.014199
31737_at	Cluster Incl J00068: Human adult skeletal muscle alpha-actin mRNA /cds=(103,1236) /gb=J00068 /gi=178028 /ug=Hs.1288 /len=1374	0.304080909	0.002586
33678_i_a	Cluster Incl X02344: Homo sapiens beta 2 gene /cds=(0,1337) /gb=X02344 /gi=37493 /ug=Hs.184582 /len=1338	0.303098003	0.003362
38086_at	Cluster Incl AB007935: Homo sapiens mRNA for KIAA0466 protein, partial cds /cds=(0,2104) /gb=AB007935 /gi=3413893 /ug=Hs.81234 /len=4974	0.303085926	0.000129
36040_at	Cluster Incl A1337192: qx88h10.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2009635 /clone_end=3" /gb=A1337192 /gi=4074119 /ug=Hs.47438 /len=925"	0.302572056	0.000013
35773_i_a	Cluster Incl AA527880: nh86h10.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-965443 /clone_end=3" /gb=AA527880 /gi=2269949 /ug=Hs.561 /len=568"	0.301976692	0.000118
33369_at	Cluster Incl A1535653: P9-C4.T3.P9.D4 Homo sapiens cDNA, 3 end /clone_end=3" /gb=A1535653 /gi=4449788 /ug=Hs.223018 /len=590"	0.301863032	0.000092
40403_at	Cluster Incl Z97171: Homo sapiens GLC1A (trabecular meshwork induced glucocorticoid response) gene, exon I, joined CDS /cds=(77,1591) /gb=Z97171 /gi=2425156 /ug=Hs.78454 /len=2262	0.301281577	0.000355
36916_at	Cluster Incl X74570: H.sapiens mRNA for Gal-beta(1-3/1-4)GlcNAc alpha-2,3-sialyltransferase /cds=(162,1151) /gb=X74570 /gi=414890 /ug=Hs.75268 /len=1741	0.301200654	0
32570_at	Cluster Incl L76465: Homo sapiens NAD+-dependent 15 hydroxyprostaglandin dehydrogenase (PGDH) mRNA, complete cds /cds=(17,817) /gb=L76465 /gi=1203983 /ug=Hs.77348 /len=2518	0.300349654	0.003846
31932_f_a	Cluster Incl M90357: Human basic transcription factor 3a (BTF3a) gene /cds=(0,476) /gb=M90357 /gi=457435 /ug=Hs.166033 /len=487	0.299724858	0.000004

Table 2. U95_A Fold Change Genes (>3 over-expressed in Barrett's associated esophageal adenocarcinoma (BA), <0.33 under-expressed in BA)

Affy ID	Gene Name	Fold Change	P-value
37225_at	Cluster Incl D79994:Human mRNA for KIAA0172 gene, partial cds /cds=(0,3923) /gb=D79994 /gi=1136403 /ug=Hs.77546 /len=4792	0.297788145	0.000001
40155_at	Cluster Incl D31883:Human mRNA for KIAA0059 gene, complete cds /cds=(221,1609) /gb=D31883 /gi=505093 /ug=Hs.158203 /len=6754	0.297603964	0.000298
31605_at	Cluster Incl U72518:Human desrin-2 pseudogene mRNA, complete cds /cds=(268,798) /gb=U72518 /gi=1673523 /ug=Hs.199299 /len=1057	0.297321107	0.000296
38057_at	Cluster Incl AL049798:Human DNA sequence from clone 797M17 on chromosome 1q22-24.3. Contains the DPT gene for Dermatopontin, ESTs, an STS and GSSs /cds=(9,614) /gb=AL049798 /gi=4995638 /ug=Hs.80552 /len=1705	0.296747826	0.04127
35730_at	Cluster Incl X03350:Human mRNA for alcohol dehydrogenase beta-1-subunit (ADH1-2 allele) /cds=(72,1199) /gb=X03350 /gi=28415 /ug=Hs.4 /len=2532	0.295479632	0.001241
34642_at	Cluster Incl U28964:Human sapiens 14-3-3 protein mRNA, complete cds /cds=(126,863) /gb=U28964 /gi=899458 /ug=Hs.75103 /len=1030	0.295377674	0.00066
36133_at	Cluster Incl AL031058:Human DNA sequence from clone 512B11 on chromosome 6p24-25. Contains the Desmoplakin I (DPI) gene, ESTs, STSs and GSSs /cds=(279,8894) /gb=AL031058 /gi=3395507 /ug=Hs.74316 /len=9591	0.295336914	0.00182
41770_at	Cluster Incl AA420624:nc61c12.r1 Homo sapiens cDNA /clone=IMAGE-745750 /gb=AA420624 /gi=2094502 /ug=Hs.183109 /len=533	0.293839135	0.005885
31831_at	Cluster Incl AI88563:wn33a05.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2447216 /clone_end=3" /gb=AI88563 /gi=5593727 /ug=Hs.149098 /len=678"	0.293100784	0.000087
32242_at	Cluster Incl AL038340:DKFZp566K192_s1 Homo sapiens cDNA, 3 end /clone=DKFZp566K192 /clone_end=3" /gb=AL038340 /gi=5407591 /ug=Hs.1940 /len=746"	0.293076261	0.000031
1629_s_at	Tyrosine Phosphatase 1, Non-Receptor, Alt. Splice 3	0.292518104	0.020967
757_at	D28364 /FEATURE= /DEFINITION=HUMAI23 Human mRNA for annexin II, 5'UTR (sequence from the 5'cap to the start codon)	0.2917755	0.007341
36900_at	Cluster Incl U52426:Homo sapiens GOK (STIM1) mRNA, complete cds /cds=(565,2622) /gb=U52426 /gi=2264345 /ug=Hs.74597 /len=4040	0.291126081	0.003618
37159_at	Cluster Incl U79259:Human clone 23945 mRNA, complete cds /cds=(636,1403) /gb=U79259 /gi=1710213 /ug=Hs.10700 /len=1683	0.2910031	0.008274

Table 2. U95_A Fold Change Genes (>3 over-expressed in Barrett's associated esophageal adenocarcinoma (BA), <0.33 under-expressed in BA)

Affy ID	Gene Name	Fold Change	P-value
36105_at	Cluster Incl M18728:Human nonspecific crossreacting antigen mRNA, complete cds /cds=UNKNOWN /gb=M18728 /gi=189084 /ug=Hs.73848 /len=2533	0.290919286	0.000145
32331_at	Cluster Incl X60673:Human AK3 mRNA for adenylate kinase 3 /cds=UNKNOWN /gb=X60673 /gi=28576 /ug=Hs.182740 /len=1692	0.29044214	0.000343
37131_at	Cluster Incl AB008390:Human sapiens mRNA for neuropsin type 1, complete cds /cds=(91,873) /gb=AB008390 /gi=5672472 /ug=Hs.104570 /len=922	0.290436248	0.000002
38627_at	Cluster Incl M95585:Human hepatic leukemia factor (HLF) mRNA, complete cds /cds=(322,1209) /gb=M95585 /gi=184223 /ug=Hs.101047 /len=3865	0.288939128	0.001437
40409_at	Cluster Incl U46689:Human microsomal aldehyde dehydrogenase (ALD10) mRNA, complete cds /cds=(449,1906) /gb=U46689 /gi=1870243 /ug=Hs.159608 /len=3918	0.288681109	0.000525
41401_at	Cluster Incl U57646:Human sapiens cysteine and glycine-rich protein 2 (CSRP2) mRNA, complete cds /cds=(56,637) /gb=U57646 /gi=1373337 /ug=Hs.10526 /len=883	0.287838122	0.003583
36955_at	Cluster Incl U10362:Human GP36b glycoprotein mRNA, complete cds /cds=(0,1070) /gb=U10362 /gi=505651 /ug=Hs.75864 /len=1407	0.287754466	0.003797
34738_at	Cluster Incl L11931:Human cytosolic serine hydroxymethyltransferase (SHMT) mRNA, complete cds /cds=(24,1475) /gb=L11931 /gi=307421 /ug=Hs.239644 /len=1669	0.285933018	0.000091
37972_at	Cluster Incl U75744:Human sapiens DNase gamma mRNA, complete cds /cds=(92,1009) /gb=U75744 /gi=3236319 /ug=Hs.88646 /len=1093	0.285701166	0.000029
32522_f a	Cluster Incl M20469:Human brain-type clathrin light-chain b mRNA, complete cds /cds=(172,861) /gb=M20469 /gi=179398 /ug=Hs.73919 /len=1134	0.285155024	0.001194
38370_at	Cluster Incl U90902:Human clone 23612 mRNA sequence /cds=UNKNOWN /gb=U90902 /gi=1913880 /ug=Hs.82141 /len=1528	0.284903455	0.000865
36079_at	Cluster Incl AF010309:Human sapiens Pig3 (PIG3) mRNA, complete cds /cds=(527,1495) /gb=AF010309 /gi=2754811 /ug=Hs.50649 /len=1670	0.28144582	0.000001
2049_s at	M29039 /FEATURE=cds /DEFINITION=HUMJUNCAA Human transactivator (jun-B) gene, complete cds	0.278175501	0.009389
41365_at	Cluster Incl Y09788:H.sapiens MUC5B gene /cds=(0,2538) /gb=Y09788 /gi=2370132 /ug=Hs.102482 /len=3100	0.275992902	0.007022

Table 2. U95_A Fold Change Genes (>3 over-expressed in Barrett's associated esophageal adenocarcinoma (BA), <0.33 under-expressed in BA)

Affy ID	Gene Name	Fold Change	P-value
31410_at	Cluster Incl AF023614: Homo sapiens transmembrane activator and CAML interactor (TACI) mRNA, complete cds /cds=(13,894) /gb=AF023614 /gi=2554947 /ug=Hs.158341 /len=1357	0.275927919	0.001766
39631_at	Cluster Incl U52100: Human XMP mRNA, complete cds /cds=(63,566) /gb=U52100 /gi=2474095 /ug=Hs.29191 /len=690	0.275453313	0.000281
32275_at	Cluster Incl X04470: Human mRNA for antileukoprotease (ALP) from cervix uterus /cds=(18,416) /gb=X04470 /gi=28638 /ug=Hs.169793 /len=594	0.273498414	0.003954
37723_at	Cluster Incl U47414: Human cyclin G2 mRNA, complete cds /cds=(135,1169) /gb=U47414 /gi=1335886 /ug=Hs.79069 /len=2044	0.273304688	0.015963
35330_at	Cluster Incl AJ012737: Homo sapiens mRNA for filamin, muscle isoform /cds=(18,8096) /gb=AJ012737 /gi=5419654 /ug=Hs.58414 /len=8842	0.273256372	0.006517
179_at	U38980 /FEATURE= /DEFINITION=U38980 Human PMS2 related (HPMSR6) mRNA, complete cds	0.271809973	0.001563
37926_at	Cluster Incl D14520: Human mRNA for GC-Box binding protein BTEB2, complete cds /cds=(558,1217) /gb=D14520 /gi=303596 /ug=Hs.84728 /len=1301	0.270544367	0.000116
32847_at	Cluster Incl U48959: Homo sapiens myosin light chain kinase (MLCK) mRNA, complete cds /cds=(119,5863) /gb=U48959 /gi=1377819 /ug=Hs.211582 /len=5926	0.270328396	0.006524
2094_s_at	K00650 /FEATURE=cds /DEFINITION=HUMFOS Human fos proto-oncogene (c-fos), complete cds	0.270175289	0.000004
467_at	U63717 /FEATURE= /DEFINITION=HSU63717 Homo sapiens osteoclast stimulating factor mRNA, complete cds	0.27004121	0.000962
36524_at	Cluster Incl AB029035: Homo sapiens mRNA for KIAA1112 protein, partial cds /cds=(0,2086) /gb=AB029035 /gi=5689560 /ug=Hs.6066 /len=3800	0.262861548	0.00005
38971_r_a	Cluster Incl AJ011896: Homo sapiens mRNA for HIV-1, Nef-associated factor 1 beta (Naf1 beta) /cds=(110,2017) /gb=AJ011896 /gi=3758820 /ug=Hs.109281 /len=2710	0.261633057	0.029949
AFFX-HU	M33197 Human glyceraldehyde-3-phosphate dehydrogenase (GAPDH) mRNA, complete cds (5, _M, 3 represent transcript regions 5 prime, Middle, and 3 prime respectively)	0.261185115	0.015471
39528_at	Cluster Incl L24564: Human Rad mRNA, complete cds /cds=(123,1049) /gb=L24564 /gi=439602 /ug=Hs.1027 /len=1443	0.260631274	0.000003
36734_at	Cluster Incl M21302: Human small proline rich protein (sprl) mRNA, clone 174N /cds=(60,278) /gb=M21302 /gi=338424 /ug=Hs.56306 /len=683	0.257892687	0

Table 2. U95_A Fold Change Genes (>3 over-expressed in Barrett's associated esophageal adenocarcinoma (BA), <0.33 under-expressed in BA)

Affy ID	Gene Name	Fold Change	P-value
33849_at	Cluster Incl U02020:Human pre-B cell enhancing factor (PBEF) mRNA, complete cds /cds=(27,1502) /gb=U02020 /gi=404012 /ug=Hs.239138 /len=2376	0.256441757	0.010246
34951_at	Cluster Incl D10923:Human mRNA for HM74 /cds=(60,1223) /gb=D10923 /gi=219866 /ug=Hs.137555 /len=2041	0.254262997	0.000014
41198_at	Cluster Incl AF055008:Homo sapiens clone 24720 epithelin 1 and 2 mRNA, complete cds /cds=(62,1843) /gb=AF055008 /gi=3005729 /ug=Hs.180577 /len=2148	0.254025212	0.000352
34281_at	Cluster Incl AF039555:Homo sapiens visinin-like protein 1 (VSNL1) mRNA, complete cds /cds=(192,767) /gb=AF039555 /gi=4104813 /ug=Hs.2288 /len=1559	0.25338608	0.015165
34198_at	Cluster Incl U12128:Human protein tyrosine phosphatase 1E (PTP1E) mRNA, complete cds /cds=(217,7689) /gb=U12128 /gi=557287 /ug=Hs.211595 /len=8287	0.252855276	0.004144
41043_at	Cluster Incl AB006867:Homo sapiens mRNA for hSOX20 protein, complete cds /cds=(494,1195) /gb=AB006867 /gi=3061309 /ug=Hs.95582 /len=1394	0.2523451	0.000279
36873_at	Cluster Incl D16532:Human gene for very low density lipoprotein receptor, 5flanking and /cds=(615,3236) /gb=D16532 /gi=407220 /ug=Hs.73729 /len=3853"	0.252075639	0.011366
34933_at	Cluster Incl AJ238381:Homo sapiens pax9 gene, exons 1-2 and joined CDS /cds=(391,1416) /gb=AJ238381 /gi=4699895 /ug=Hs.132576 /len=1630	0.251978856	0.043656
34651_at	Cluster Incl M58525:Homo sapiens catechol-O-methyltransferase (COMT) mRNA, complete cds /cds=(204,1019) /gb=M58525 /gi=179954 /ug=Hs.78534 /len=1206	0.250728594	0.000702
32527_at	Cluster Incl AI381790:te41h10.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2089315 /clone_end=3" /gb=AI381790 /gi=4194571 /ug=Hs.74120 /len=544"	0.250563902	0.014061
38903_at	Cluster Incl AF099731:Homo sapiens connexin 31.1 (GJB5) gene, complete cds /cds=(27,848) /gb=AF099731 /gi=4009521 /ug=Hs.198249 /len=1370	0.249028452	0.000008
32112_s	Cluster Incl AI800499:tc11f11.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2063565 /clone_end=3" /gb=AI800499 /gi=5365971 /ug=Hs.161002 /len=403"	0.248564076	0.000001
36838_at	Cluster Incl AF055481:Homo sapiens normal epithelial cell-specific 1 (NES1) gene, complete cds /cds=(82,912) /gb=AF055481 /gi=3065710 /ug=Hs.69423 /len=1442	0.248424399	0.001939
32163_f_a	Cluster Incl AA216639:zq95f07.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-649765 /clone_end=3" /gb=AA216639 /gi=1817337 /ug=Hs.184093 /len=569"	0.247712958	0.010541

Table 2. U95_A Fold Change Genes (>3 over-expressed in Barrett's associated esophageal adenocarcinoma (BA), <0.33 under-expressed in BA)

Affy ID	Gene Name	Fold Change	P-value
32200_at	Cluster Incl M24902:Human prostatic acid phosphatase mRNA, complete cds /cds=(23,1183) /gb=M24902 /gi=189618 /ug=Hs.1852 /len=3097	0.247567897	0.009707
38881_i_a	Cluster Incl AF096870:Homo sapiens estrogen-responsive B box protein (EBBP) mRNA, complete cds /cds=(227,1921) /gb=AF096870 /gi=3916726 /ug=Hs.194540 /len=2568	0.245430421	0.000297
39171_at	Cluster Incl W21787:58b10 Homo sapiens cDNA /clone=(not-directional) /gb=W21787 /gi=1298717 /ug=Hs.99816 /len=775	0.24193833	0.000959
31655_at	Cluster Incl AL031737:Human DNA sequence from clone 8B22 on chromosome 1p35.1-36.21 Contains gene similar to cytoplasmic dynein light chain 1, GSSs /cds=(92,361) /gb=AL031737 /gi=4464258 /ug=Hs.225980 /len=371	0.240900298	0.027265
37215_at	Cluster Incl AF046798:untitled /cds=(113,2656) /gb=AF046798 /gi=3170406 /ug=Hs.771 /len=2828	0.240324439	0.000027
38339_at	Cluster Incl AF082868:Homo sapiens gamma butyrobetaine hydroxylase (BBH) mRNA, complete cds /cds=(66,1229) /gb=AF082868 /gi=3746804 /ug=Hs.9667 /len=1584	0.238959561	0.000097
35803_at	Cluster Incl S82240:RhoE=26 kDa GTPase homolog [human, HeLa cell line, mRNA, 833 nt] /cds=(24,713) /gb=S82240 /gi=1839516 /ug=Hs.6838 /len=833	0.238923582	0.005486
40096_at	Cluster Incl D14710:Human mRNA for ATP synthase alpha subunit, complete cds /cds=(63,1724) /gb=D14710 /gi=559324 /ug=Hs.155101 /len=1857	0.234166294	0.016171
36890_at	Cluster Incl AF001691:Homo sapiens 195 kDa cornified envelope precursor mRNA, complete cds /cds=(90,5360) /gb=AF001691 /gi=3168845 /ug=Hs.74304 /len=6227	0.233555948	0.020797
39052_at	Cluster Incl J00124:Homo sapiens 50 kDa type I epidermal keratin gene, complete cds /cds=(61,1479) /gb=J00124 /gi=186704 /ug=Hs.117729 /len=1634	0.231924773	0.03245
32010_at	Cluster Incl Z82180:Human DNA sequence from clone E81G9 on chromosome 22 Contains novel gene EAN57, ESTs and GSS /cds=(0,181) /gb=Z82180 /gi=5051358 /ug=Hs.225954 /len=285	0.231601307	0.000002
41469_at	Cluster Incl L10343:Huma elafin gene, complete cds /cds=(516,869) /gb=L10343 /gi=190337 /ug=Hs.112341 /len=871	0.231452377	0.00149
35909_at	Cluster Incl Z50194:H.sapiens mRNA for PQ-rich protein /cds=(159,1361) /gb=Z50194 /gi=929659 /ug=Hs.198179 /len=1412	0.231034761	0.003707
36555_at	Cluster Incl AF044311:Homo sapiens gamma-synuclein gene, complete cds /cds=(52,435) /gb=AF044311 /gi=3347841 /ug=Hs.63236 /len=708	0.230334156	0.013692

Table 2. U95_A Fold Change Genes (>3 over-expressed in Barrett's associated esophageal adenocarcinoma (BA), <0.33 under-expressed in BA)

Affy ID	Gene Name	Fold Change	P-value
1582_at	M29540 /FEATURE= /DEFINITION=HUMCEAF Human carcinoembryonic antigen mRNA (CEA), complete cds	0.228698047	0.000018
39248_at	Cluster Incl N74607:za55a01.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-296424 /clone_end=3" /gb=N74607 /gi=1231892 /ug=Hs.234642 /len=487"	0.227986593	0.00066
33370_r_a	Cluster Incl U60205:Human methyl sterol oxidase (ERG25) mRNA, complete cds /cds=(26,907) /gb=U60205 /gi=1408205 /ug=Hs.223018 /len=1751	0.22574526	0.000114
32392_s	Cluster Incl M57951:Human bilirubin UDP-glucuronosyltransferase isozyme 2 mRNA, complete cds /cds=(29,1633) /gb=M57951 /gi=184474 /ug=Hs.233441 /len=2368	0.221926907	0.005613
40303_at	Cluster Incl U85658:Human transcription factor ERF-1 mRNA, complete cds /cds=(166,1518) /gb=U85658 /gi=2058552 /ug=Hs.61796 /len=2785	0.220714707	0.000106
37157_at	Cluster Incl X56667:Human mRNA for calretinin /cds=(43,858) /gb=X56667 /gi=29635 /ug=Hs.106857 /len=1426	0.219711115	0.000083
234_s_at	M57399 /FEATURE= /DEFINITION=HUMHBNF1 Human nerve growth factor (HBNF-1) mRNA, complete cds	0.213743207	0.002063
33792_at	Cluster Incl AF043498:Homo sapiens prostate stem cell antigen (PSCA) mRNA, complete cds /cds=(17,388) /gb=AF043498 /gi=2909843 /ug=Hs.20166 /len=990	0.212093464	0
37765_at	Cluster Incl X54162:Human mRNA for a 64 Kd autoantigen expressed in thyroid and extra-ocular muscle /cds=(212,1930) /gb=X54162 /gi=28968 /ug=Hs.79386 /len=3849	0.21133549	0.027383
31542_at	Cluster Incl M60502:Human profilaggrin mRNA, 3 end /cds=(0,2393) /gb=M60502 /gi=190403 /ug=Hs.73995 /len=2930"	0.209204984	0.000756
33128_s	Cluster Incl W68521:zd36f07.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-342757 /clone_end=5" /gb=W68521 /gi=1377410 /ug=Hs.83393 /len=579"	0.205685908	0.000172
36242_at	Cluster Incl M21539:Human small proline rich protein (sprl1) mRNA, clone 1292 /cds=(86,304) /gb=M21539 /gi=338426 /ug=Hs.2421 /len=678	0.202617237	0.000204
33883_at	Cluster Incl AB001466:Homo sapiens mRNA for Efs1, complete cds /cds=(608,2293) /gb=AB001466 /gi=2829301 /ug=Hs.24587 /len=3114	0.201124632	0.001354
32582_at	Cluster Incl AF001548:Human Chromosome 16 BAC clone CIT987SK-A-815A9 /cds=(0,5573) /gb=AF001548 /gi=2104552 /ug=Hs.78344 /len=6428	0.198342888	0.001142
1913_at	U47414 /FEATURE= /DEFINITION=HSU47414 Human cyclin G2 mRNA, complete cds	0.197140492	0.000035

Table 2. U95_A Fold Change Genes (>3 over-expressed in Barrett's associated esophageal adenocarcinoma (BA), <0.33 under-expressed in BA)

Affy ID	Gene Name	Fold Change	P-value
34203_at	Cluster Incl D17408: Homo sapiens mRNA for calponin, complete cds /cds=(92,985) /gb=D17408 /gi=1783204 /ug=Hs.21223 /len=1517	0.195771996	0.000225
32963_s	Cluster Incl W27549:32d11 Homo sapiens cDNA /gb=W27549 /gi=1307353 /ug=Hs.235634 /len=912	0.193598948	0.000017
1165_at	D49950 /FEATURE= /DEFINITION=D49950 Homo sapiens mRNA for interferon-gamma inducing factor(IGIF), complete cds	0.191184898	0.000062
1005_at	X68277 /FEATURE=cds /DEFINITION=HSCL100 H.sapiens CL 100 mRNA for protein tyrosine phosphatase	0.190308395	0.008438
32523_at	Cluster Incl M20470: Human lymphocyte clathrin light-chain B mRNA, complete cds /cds=(139,774) /gb=M20470 /gi=187056 /ug=Hs.73919 /len=1051	0.189040488	0.005713
40016_g	Cluster Incl AB002301: Human mRNA for KIAA0303 gene, partial cds /cds=(0,6415) /gb=AB002301 /gi=2224546 /ug=Hs.54985 /len=6629	0.188340227	0.000827
35425_at	Cluster Incl AJ243512: Homo sapiens mRNA for Barx2 protein (Barx2 gene) /cds=(16,855) /gb=AJ243512 /gi=5459378 /ug=Hs.167218 /len=1374	0.187189147	0.000087
2027_at	M87068 /FEATURE= /DEFINITION=HUMCAN H.sapiens CaN19 mRNA sequence	0.187103745	0.000726
36925_at	Cluster Incl L26336: Human heat shock protein HSPA2 gene, complete cds /cds=(0,1919) /gb=L26336 /gi=476704 /ug=Hs.75452 /len=1920	0.182654009	0.000097
39015_f.a	Cluster Incl L42611: Homo sapiens keratin 6 isoform K6e (KRT6E) mRNA, complete cds /cds=(40,1734) /gb=L42611 /gi=908802 /ug=Hs.111758 /len=1986	0.181632277	0.020188
613_at	M21389 /FEATURE=mRNA /DEFINITION=HUMKER2A Human keratin type II (58 kD) mRNA, complete cds	0.175195643	0.035399
36378_at	Cluster Incl AF085807: Homo sapiens uroplakin Ia mRNA, partial cds /cds=(0,771) /gb=AF085807 /gi=3550409 /ug=Hs.159309 /len=1218	0.174269851	0.000023
31846_at	Cluster Incl AW003733: ws16b04.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2497327 /clone_end=3" /gb=AW003733 /gi=5850649 /ug=Hs.15114 /len=839"	0.167432167	0.010423
1197_at	D00654 /FEATURE=cds /DEFINITION=HUMACTSG7 Homo sapiens gene for enteric smooth muscle gamma-actin, exon9, complete cds	0.163684848	0.009945
31343_at	Cluster Incl AJ005835: Homo sapiens mRNA for interleukin 1 receptor antagonist, type III /cds=(0,10) /gb=AJ005835 /gi=3115205 /ug=Hs.131958 /len=171	0.16202207	0.000012

Table 2. U95_A Fold Change Genes (>3 over-expressed in Barrett's associated esophageal adenocarcinoma (BA), <0.33 under-expressed in BA)

Affy ID	Gene Name	Fold Change	P-value
37576_at	Cluster Incl U52969:Human PEP19 (PCP4) mRNA, complete cds /cds=(81,269) /gb=U52969 /gi=1568614 /ug=Hs.80296 /len=554	0.160690395	0.000535
2090_i_at	H12458 /FEATURE= /DEFINITION=H12458 y12d03.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:148517 3" similar to SP:WNT6_MOUSE P22727 WNT-6 PROTEIN ; mRNA sequence	0.159035469	0.01138
33331_at	Cluster Incl U17077:Human BENE mRNA, partial cds /cds=(0,446) /gb=U17077 /gi=1000711 /ug=Hs.185055 /len=2269	0.156306005	0.000286
40035_at	Cluster Incl AB012917:Homo sapiens mRNA for serine protease (TLSP), complete cds /cds=(25,873) /gb=AB012917 /gi=3649790 /ug=Hs.57771 /len=1186	0.15559402	0.002195
39660_at	Cluster Incl AI309115:q071a09.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1913944 /clone_end=3" /gb=AI309115 /gi=4003986 /ug=Hs.32949 /len=450"	0.155477892	0.000234
33546_at	Cluster Incl AI923984:wn49d12.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2448791 /clone_end=3" /gb=AI923984 /gi=5659948 /ug=Hs.46320 /len=440"	0.155471597	0.009457
41471_at	Cluster Incl W72424 /gi=1382379 /ug=Hs.112405 /len=604" /gb=W72424 /gi=1382379 /ug=Hs.112405 /len=604"	0.15508022	0.018334
33483_at	Cluster Incl X76029:H.sapiens mRNA for neuromedin U /cds=(105,629) /gb=X76029 /gi=609012 /ug=Hs.2841 /len=817	0.154692443	0.022939
39682_at	Cluster Incl X87159:H.sapiens mRNA for beta subunit of epithelial amiloride-sensitive sodium channel /cds=(127,2049) /gb=X87159 /gi=1004270 /ug=Hs.37129 /len=2545	0.154579413	0.000005
617_at	M24902 /FEATURE=mRNA /DEFINITION=HUMPAPA Human prostatic acid phosphatase mRNA, complete cds	0.153293459	0
34820_at	Cluster Incl M57399:Human nerve growth factor (HBNF-1) mRNA, complete cds /cds=(395,901) /gb=M57399 /gi=292072 /ug=Hs.44 /len=1029	0.152145671	0.000666
36454_at	Cluster Incl AF037335:Homo sapiens carbonic anhydrase precursor (CA 12) mRNA, complete cds /cds=(115,1179) /gb=AF037335 /gi=2708638 /ug=Hs.5338 /len=2755	0.151522134	0.001281
39544_at	Cluster Incl AB002351:Human mRNA for KIAA0353 gene, partial cds /cds=(0,4125) /gb=AB002351 /gi=2224646 /ug=Hs.10587 /len=6651	0.148964837	0.01262
40365_at	Cluster Incl M63904:Human G-alpha 16 protein mRNA, complete cds /cds=(219,1343) /gb=M63904 /gi=182891 /ug=Hs.73797 /len=2060	0.148225853	0.000153

Table 2. U95_A Fold Change Genes (>3 over-expressed in Barrett's associated esophageal adenocarcinoma (BA), <0.33 under-expressed in BA)

Affy ID	Gene Name	Fold Change	P-value
37160_at	Cluster Incl M19888:Human small proline rich protein (spr1) mRNA, clone 128 /cds=(68,337) /gb=M19888 /gi=338416 /ug=Hs.1076 /len=623	0.145719365	0.000021
529_at	U15932 /FEATURE= /DEFINITION=HSU15932 Human dual-specificity protein phosphatase mRNA, complete cds	0.144995121	0.000002
770_at	D00632 /FEATURE= /DEFINITION=HUMGSHPX Homo sapiens mRNA for glutathione peroxidase, complete cds	0.143850665	0.002402
31805_at	Cluster Incl M64347:Human novel growth factor receptor mRNA, 3 cds /cds=(0,2195) /gb=M64347 /gi=182564 /ug=Hs.1420 /len=3799"	0.14334791	0.000421
41034_s	Cluster Incl U92315:Homo sapiens hydroxysteroid sulfotransferase SUL12B1b (HSST2) mRNA, complete cds /cds=(81,1178) /gb=U92315 /gi=1923292 /ug=Hs.94581 /len=1199	0.143222232	0.000049
37600_at	Cluster Incl U68186:Human extracellular matrix protein 1 mRNA, complete cds /cds=(103,1725) /gb=U68186 /gi=2660683 /ug=Hs.81071 /len=1819	0.141941707	0.000773
37762_at	Cluster Incl Y07909:H sapiens mRNA for Progression Associated Protein /cds=(218,691) /gb=Y07909 /gi=1542882 /ug=Hs.79368 /len=2774	0.141800128	0.001618
35726_at	Cluster Incl A1539439:te51e07.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2090244 /clone_end=3" /gb=A1539439 /gi=4453574 /ug=Hs.38991 /len=455"	0.141239149	0.000072
39302_at	Cluster Incl X56807:Human DSC2 mRNA for desmocollins type 2a and 2b /cds=(0,2583) /gb=X56807 /gi=30507 /ug=Hs.239727 /len=3212	0.14069071	0.000006
37920_at	Cluster Incl U70370:Human hindlimb expressed homeobox protein backfoot (Bff) mRNA, complete cds /cds=(111,1055) /gb=U70370 /gi=1870670 /ug=Hs.84136 /len=2049	0.139179451	0.000061
39698_at	Cluster Incl U51712:HSU51712 Homo sapiens cDNA /gb=U51712 /gi=1255282 /ug=Hs.13775 /len=1110	0.13905098	0.000053
36497_at	Cluster Incl W28438:47g10 Homo sapiens cDNA /gb=W28438 /gi=1308449 /ug=Hs.57548 /len=845	0.136810256	0.005909
601_s_at	M28439 /FEATURE=cds /DEFINITION=HUMKER16A8 Human keratin type 16 gene, exon 8	0.136363596	0.003168
36658_at	Cluster Incl D13643:Human mRNA for KIAA0018 gene, complete cds /cds=(38,1210) /gb=D13643 /gi=285996 /ug=Hs.75616 /len=4186	0.135965128	0.008011
38202_at	Cluster Incl AB011535:Homo sapiens mRNA for MEGF1, partial cds /cds=(0,1721) /gb=AB011535 /gi=3449295 /ug=Hs.158159 /len=3193	0.129294854	0.000014

Table 2. U95_A Fold Change Genes (>3 over-expressed in Barrett's associated esophageal adenocarcinoma (BA), <0.33 under-expressed in BA)

Affy ID	Gene Name	Fold Change	P-value
37603_at	Cluster Incl X52015:H.sapiens mRNA for interleukin-1 receptor antagonist /cds=(23,556) /gb=X52015 /gi=32576 /ug=Hs.81134 /len=1740	0.128827966	0.000242
32113_at	Cluster Incl U83115:Human non-lens beta gamma-crystallin like protein (AIM1) mRNA, partial cds /cds=(0,4913) /gb=U83115 /gi=2072424 /ug=Hs.161002 /len=6796	0.124007546	0.000013
39366_at	Cluster Incl N36638:yx88f05.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-268833 /clone_end=5" /gb=N36638 /gi=1157780 /ug=Hs.12112 /len=543"	0.123584314	0.000028
40304_at	Cluster Incl M69225:Human bullous pemphigoid antigen (BPAG1) mRNA, complete cds /cds=UNKNOWN /gb=M69225 /gi=179522 /ug=Hs.620 /len=8930	0.121641611	0
37473_at	Cluster Incl AF061812:Homo sapiens keratin 16 (KRT16A) mRNA, complete cds /cds=(14,1435) /gb=AF061812 /gi=4091878 /ug=Hs.115947 /len=1588	0.120176887	0.002993
1776_at	L24564 /FEATURE= /DEFINITION=HUMRAD Human Rad mRNA, complete cds	0.119942667	0.000005
38051_at	Cluster Incl X76220:H.sapiens MAL gene exon 1 (and joined CDS) /cds=(59,520) /gb=X76220 /gi=433225 /ug=Hs.80395 /len=1056	0.118545163	0.015366
37956_at	Cluster Incl U37519:Human aldehyde dehydrogenase (ALDH8) mRNA, complete cds /cds=(616,1773) /gb=U37519 /gi=1051280 /ug=Hs.87539 /len=2827	0.114940468	0.000183
39569_at	Cluster Incl U72849:untitled /cds=(98,6199) /gb=U72849 /gi=4097997 /ug=Hs.25482 /len=6457	0.113225316	0.000035
40356_at	Cluster Incl AB026833:Homo sapiens mRNA for chloride channel protein, complete cds /cds=(41,2872) /gb=AB026833 /gi=4887600 /ug=Hs.72365 /len=3604	0.109385318	0.000001
37093_at	Cluster Incl M32402:Human placental protein (PP11) mRNA, complete cds /cds=UNKNOWN /gb=M32402 /gi=190210 /ug=Hs.997 /len=2320	0.103523453	0.000448
1321_s_at	U43916 /FEATURE= /DEFINITION=HSU43916 Human tumor-associated membrane protein homolog (TMP) mRNA, complete cds	0.102454011	0
36284_at	Cluster Incl Y12642:H.sapiens E48 gene /cds=(24,410) /gb=Y12642 /gi=2739293 /ug=Hs.3185 /len=748	0.101688161	0.000003
774_g_at	D10667 /FEATURE= /DEFINITION=HUMMHCAAA Homo sapiens mRNA for smooth muscle myosin heavy chain, partial cds	0.098993518	0.004537
1898_at	L24203 /FEATURE= /DEFINITION=HUMDK Homo sapiens ataxia-telangiectasia group D-associated protein mRNA, complete cds	0.097775137	0.000124

Table 2. U95_A Fold Change Genes (>3 over-expressed in Barrett's associated esophageal adenocarcinoma (BA), <0.33 under-expressed in BA)

Affy ID	Gene Name	Fold Change	P-value
41783_at	Cluster Incl M97815:Human retinoic acid-binding protein II (CRABP-II) gene /cds=(137,553) /gb=M97815 /gi=181029 /ug=Hs.183650 /len=969	0.097133202	0.000064
773_at	D10667 /FEATURE= /DEFINITION=HUMMHCAAA Homo sapiens mRNA for smooth muscle myosin heavy chain, partial cds	0.095787941	0.005341
41641_at	Cluster Incl AJ223603:Homo sapiens mRNA encoding rat C4.4-like protein /cds=(86,1126) /gb=AJ223603 /gi=3821054 /ug=Hs.11950 /len=1684	0.095093025	0.000087
40776_at	Cluster Incl M63391:Human desmin gene, complete cds /cds=(80,1489) /gb=M63391 /gi=181539 /ug=Hs.171185 /len=2220	0.094099776	0.000018
862_at	U04313 /FEATURE= /DEFINITION=HSU04313 Human maspin mRNA, complete cds	0.091970059	0.000527
33693_at	Cluster Incl M76482:Human 130-kD pemphigus vulgaris antigen mRNA, complete cds /cds=(83,3082) /gb=M76482 /gi=190751 /ug=Hs.1925 /len=3336	0.091756719	0.000006
36464_at	Cluster Incl X94323:H.sapiens mRNA for SGP28 protein /cds=(40,777) /gb=X94323 /gi=1213612 /ug=Hs.54431 /len=2124	0.088981309	0.000056
35124_at	Cluster Incl M62982:Human arachidonate 12-lipoxygenase mRNA, complete cds /cds=(53,2044) /gb=M62982 /gi=177106 /ug=Hs.1200 /len=2348	0.087650494	0.004249
1057_at	M97815 /FEATURE=expanded_cds /DEFINITION=HUMCRABP02 Human retinoic acid-binding protein II (CRABP-II) gene exons 2-4, complete cds	0.084318624	0.000101
31345_at	Cluster Incl AB002134:Homo sapiens mRNA for airway trypsin-like protease, complete cds /cds=(61,1317) /gb=AB002134 /gi=3184183 /ug=Hs.132195 /len=1500	0.082579556	0.013315
1549_s_at	U19557 /FEATURE= /DEFINITION=HSU19557 Human squamous cell carcinoma antigen 2 (SCCA2) mRNA, complete cds	0.08107938	0.000031
31791_at	Cluster Incl Y16961:Homo sapiens mRNA for KET protein /cds=(27,2069) /gb=Y16961 /gi=3970716 /ug=Hs.137569 /len=4849	0.079103695	0.009833
1343_s_at	S66896 /FEATURE= /DEFINITION=S66896 squamous cell carcinoma antigen=serine protease inhibitor [human, mRNA, 1711 nt]	0.07050762	0.000109
36355_at	Cluster Incl M13903:Human involucrin mRNA /cds=(0,1757) /gb=M13903 /gi=186520 /ug=Hs.157091 /len=1758	0.063600753	0.000334
40315_at	Cluster Incl AJ228139:Homo sapiens mRNA for LETK1 precursor /cds=(43,3237) /gb=AJ228139 /gi=4585698 /ug=Hs.64867 /len=3528	0.063426329	0.001565

Table 2. U95_A Fold Change Genes (>3 over-expressed in Barrett's associated esophageal adenocarcinoma (BA), <0.33 under-expressed in BA)

Affy ID	Gene Name	Fold Change	P-value
37582_at	Cluster Incl X07696:Human mRNA for cytokeratin 15 /cds=(61,1431) /gb=X07696 /gi=34070 /ug=Hs.80342 /len=1709	0.063223853	0.00109
36406_at	Cluster Incl AA401397:zu68b01.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-743113 /clone_end=3" /gb=AA401397 /gi=2053605 /ug=Hs.165296 /len=519"	0.06095209	0.000001
40031_at	Cluster Incl M74542:Human aldehyde dehydrogenase type III (ALDHIII) mRNA, complete cds /cds=(42,1403) /gb=M74542 /gi=178401 /ug=Hs.575 /len=1636	0.058614393	0.000689
37954_at	Cluster Incl X16662:Human mRNA for vascular anticoagulant-beta (VAC-beta) /cds=(106,1089) /gb=X16662 /gi=37638 /ug=Hs.87268 /len=1940	0.058021351	0.000785
32139_at	Cluster Incl Y09538:H.sapiens mRNA for ZNF185 gene /cds=(40,1398) /gb=Y09538 /gi=2370125 /ug=Hs.16622 /len=3604	0.057956613	0.000018
37185_at	Cluster Incl Y00630:Human mRNA for Arg-Serpin (plasminogen activator-inhibitor 2, PAI-2) /cds=(72,1319) /gb=Y00630 /gi=35267 /ug=Hs.75716 /len=1900	0.057481589	0.005043
39581_at	Cluster Incl AA570193:mf38c11.s1 Homo sapiens cDNA /clone=IMAGE-916052 /gb=AA570193 /gi=2344173 /ug=Hs.2621 /len=450	0.057372976	0.003457
36407_at	Cluster Incl AL050220:Homo sapiens mRNA; cDNA DKFZp586J1923 (from clone DKFZp586J1923) /cds=(0,590) /gb=AL050220 /gi=4884461 /ug=Hs.165296 /len=733	0.056802495	0.000001
39249_at	Cluster Incl AB001325:Human AQP3 gene for aquaporine 3 (water channel), partial cds /cds=(60,938) /gb=AB001325 /gi=1854373 /ug=Hs.234642 /len=1442	0.049433675	0.000144
38489_at	Cluster Incl M60047:Human heparin binding protein (HBp17) mRNA, complete cds /cds=(97,801) /gb=M60047 /gi=183950 /ug=Hs.1690 /len=1146	0.048264708	0.000019
33529_at	Cluster Incl X76342:H.sapiens ADH7 mRNA /cds=UNKNOWN /gb=X76342 /gi=541674 /ug=Hs.389 /len=2055	0.048228074	0
35947_at	Cluster Incl M98447:H.sapiens keratinocyte transglutaminase gene, complete cds /cds=(90,2543) /gb=M98447 /gi=186734 /ug=Hs.22 /len=2719	0.04499404	0.045596
35105_at	Cluster Incl AF045941:Homo sapiens scellin (SCEL) mRNA, complete cds /cds=(86,2092) /gb=AF045941 /gi=3893854 /ug=Hs.115166 /len=2327	0.040865578	0.022763
32868_at	Cluster Incl L10386:Homo sapiens transglutaminase E3 (TGASE3) mRNA, complete cds /cds=(41,2122) /gb=L10386 /gi=307503 /ug=Hs.2022 /len=2619	0.039911624	0.000146

Table 2. U95_A Fold Change Genes (>3 over-expressed in Barrett's associated esophageal adenocarcinoma (BA), <0.33 under-expressed in BA)

Affy ID	Gene Name	Fold Change	P-value
31705_at	Cluster Incl X99977:H.sapiens ARS gene, component B /cds=(26,337) /gb=X99977 /gi=1536901 /ug=Hs.103505 /len=528	0.028363962	0.000051
38608_at	Cluster Incl AA010777:ze22f06.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-359747 /clone_end=5" /gb=AA010777 /gi=1471804 /ug=Hs.99923 /len=521"	0.028030428	0.000245

Table 3. U95_B Fold Change Genes (>3 over-expressed in Barrett's associated esophageal adenocarcinoma (BA), <0.33 under-expressed in BA)

Affy ID	Gene Name	Fold Change	P-value
55905_g_a	Cluster Incl. AW007803:wt03d03.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2506373 /clone_end=3' /gb=AW007803 /gi=5856581 /ug=Hs.61311 /len=544'	51.27773413	0.000037
47862_at	Cluster Incl. AA158234:zo76b01.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-592777 /clone_end=3' /gb=AA158234 /gi=1733029 /ug=Hs.72222 /len=614'	22.47041512	0.00011
51811_at	Cluster Incl. AA535447:nf84h07.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-926653 /clone_end=3' /gb=AA535447 /gi=2279700 /ug=Hs.5366 /len=524'	18.5502306	0.000002
49252_at	Cluster Incl. R40393:yf71c01.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-27679 /clone_end=3' /gb=R40393 /gi=822823 /ug=Hs.239147 /len=485'	15.5072013	0.000108
55610_at	Cluster Incl. A1742239:wg39e09.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2367496 /clone_end=3' /gb=A1742239 /gi=5110527 /ug=Hs.91109 /len=493'	14.88983284	0.000003
46682_at	Cluster Incl. A1985652:wt19b08.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2507895 /clone_end=3' /gb=A1985652 /gi=5812929 /ug=Hs.7362 /len=539'	14.5125698	0.000036
45204_s_at	Cluster Incl. A1378647:tc57a04.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2068686 /clone_end=3' /gb=A1378647 /gi=4188500 /ug=Hs.42502 /len=481'	12.18224933	0.000011
54001_at	Cluster Incl. A1092936:qa81b05.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1693137 /clone_end=3' /gb=A1092936 /gi=3431912 /ug=Hs.6459 /len=516'	11.81231717	0.000235
45294_at	Cluster Incl. A1697470:tt08h01.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2208241 /clone_end=3' /gb=A1697470 /gi=4985370 /ug=Hs.205126 /len=494'	10.79542287	0.002361
46165_at	Cluster Incl. AA001552:ze46c08.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-362030 /clone_end=3' /gb=AA001552 /gi=1437017 /ug=Hs.59839 /len=566'	9.689374943	0.000026
44558_at	Cluster Incl. A1148745:qc69e03.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1714876 /clone_end=3' /gb=A1148745 /gi=3677214 /ug=Hs.30715 /len=733'	9.603193191	0.000001
56495_at	Cluster Incl. A1301060:qp16c05.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1908680 /clone_end=3' /gb=A1301060 /gi=3960406 /ug=Hs.11365 /len=618'	8.981853987	0.000031
47475_at	Cluster Incl. A1057608:oy31e08.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1667462 /clone_end=3' /gb=A1057608 /gi=3331474 /ug=Hs.127826 /len=657'	7.95757126	0.001394

Table 3. U95_B Fold Change Genes (>3 over-expressed in Barrett's associated esophageal adenocarcinoma (BA), <0.33 under-expressed in BA)

Affy ID	Gene Name	Fold Change	P-value
53718_at	Cluster Incl. AI684645:wa84h12.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2302919 /clone_end=3' /gb=AI684645 /gi=4895939 /ug=Hs.12126 /len=585'	7.724496401	0.00059
42973_at	Cluster Incl. AA458524:zx96b11.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-811581 /clone_end=5' /gb=AA458524 /gi=2183431 /ug=Hs.21835 /len=470'	7.478781625	0.000217
55802_at	Cluster Incl. AW007803:wf03d03.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2506373 /clone_end=3' /gb=AW007803 /gi=5856581 /ug=Hs.61311 /len=544'	7.379846073	0.016111
46652_at	Cluster Incl. AA524036:ng32f10.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-936523 /clone_end=3' /gb=AA524036 /gi=2264964 /ug=Hs.71190 /len=608'	7.07207438	0.001998
52119_at	Cluster Incl. AA418063:zv97b02.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-767691 /clone_end=5' /gb=AA418063 /gi=2079937 /ug=Hs.44278 /len=585'	6.967128041	0.000278
54150_at	Cluster Incl. AI669065:we70d12.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2346455 /clone_end=3' /gb=AI669065 /gi=4833839 /ug=Hs.71779 /len=518'	6.834403508	0.000058
50849_at	Cluster Incl. AI922323:wn90h03.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2453141 /clone_end=3' /gb=AI922323 /gi=5658287 /ug=Hs.122576 /len=483'	6.666123575	0.000285
56122_at	Cluster Incl. AI223817:qj33d01.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1858273 /clone_end=3' /gb=AI223817 /gi=3806530 /ug=Hs.100686 /len=620'	6.326746141	0.002608
46659_at	Cluster Incl. AI742057:wg38d12.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2367383 /clone_end=3' /gb=AI742057 /gi=5110345 /ug=Hs.7155 /len=603'	6.316573114	0.000494
56806_at	Cluster Incl. AI809891:wf59e01.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2359896 /clone_end=3' /gb=AI809891 /gi=5396457 /ug=Hs.104573 /len=481'	6.165253015	0.001843
57094_at	Cluster Incl. AI189381:qd05h06.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1722875 /clone_end=3' /gb=AI189381 /gi=3740590 /ug=Hs.203125 /len=807'	6.135568271	0.000033
47060_at	Cluster Incl. AI422335:tf65f01.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2104153 /clone_end=3' /gb=AI422335 /gi=4268266 /ug=Hs.78358 /len=540'	6.055112775	0.000721
46644_at	Cluster Incl. AA523925:ng24g06.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-935770 /clone_end=3' /gb=AA523925 /gi=2264853 /ug=Hs.70732 /len=662'	6.039307564	0.000053
56904_g_a	Cluster Incl. AW004007:wq94g10.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2479746 /clone_end=3' /gb=AW004007 /gi=5850923 /ug=Hs.109257 /len=262'	6.027803262	0.000267

Table 3. U95_B Fold Change Genes (>3 over-expressed in Barrett's associated esophageal adenocarcinoma (BA), <0.33 under-expressed in BA)

Affy ID	Gene Name	Fold Change	P-value
47890_at	Cluster Incl. AI921465:wo25d05.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2456361 /clone_end=3' /gb=AI921465 /gi=5657429 /ug=Hs.146314 /len=504'	5.778899418	0.000053
57861_at	Cluster Incl. AI096493:qa03d12.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1685687 /clone_end=3' /gb=AI096493 /gi=3445987 /ug=Hs.172572 /len=586'	5.69536482	0.000123
45382_g_a	Cluster Incl. AI392817:tg10a06.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2108338 /clone_end=3' /gb=AI392817 /gi=4222364 /ug=Hs.239331 /len=543'	5.623492806	0.000069
59661_at	Cluster Incl. W81116:zh149d10.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-415411 /clone_end=3' /gb=W81116 /gi=1391615 /ug=Hs.20524 /len=622'	5.495775955	0.000252
44140_at	Cluster Incl. AA056278:zf53h03.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-380693 /clone_end=3' /gb=AA056278 /gi=1548682 /ug=Hs.28669 /len=632'	5.287393752	0.000019
48745_s_at	Cluster Incl. AI979240:wu03g12.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2515942 /clone_end=3' /gb=AI979240 /gi=5804361 /ug=Hs.233729 /len=226'	5.222721476	0.003423
45183_at	Cluster Incl. AL118812:DKFZp761G111_r1 Homo sapiens cDNA, 5 end /clone=DKFZp761G111 /clone_end=5' /gb=AL118812 /gi=5924711 /ug=Hs.41139 /len=1642'	5.057329191	0.000756
49052_at	Cluster Incl. AA147884:zl50b04.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-505327 /clone_end=3' /gb=AA147884 /gi=1717300 /ug=Hs.9812 /len=652'	4.985943579	0.001171
47522_at	Cluster Incl. AW007479:ws52c07.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2500812 /clone_end=3' /gb=AW007479 /gi=5856257 /ug=Hs.143974 /len=497'	4.974197171	0.000006
48120_at	Cluster Incl. H30385:ym58d12.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-52891 /clone_end=3' /gb=H30385 /gi=901295 /ug=Hs.11067 /len=519'	4.798932814	0.000126
46675_at	Cluster Incl. AA625199:af70e02.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-1047386 /clone_end=5' /gb=AA625199 /gi=2537584 /ug=Hs.72289 /len=566'	4.790908464	0.004853
52054_at	Cluster Incl. AI434780:ti20c05.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2131016 /clone_end=3' /gb=AI434780 /gi=4298572 /ug=Hs.4248 /len=933'	4.774162147	0.000001
46219_at	Cluster Incl. Z99410:HSZ99410 Homo sapiens cDNA /clone=DKFZphamy1_1c7 /gb=Z99410 /gi=2415650 /ug=Hs.6314 /len=669	4.7581476	0.000006
47627_at	Cluster Incl. AI445492:tj24c09.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2142448 /clone_end=3' /gb=AI445492 /gi=4288591 /ug=Hs.98370 /len=545'	4.705362783	0.006739

Table 3. U95_B Fold Change Genes (>3 over-expressed in Barrett's associated esophageal adenocarcinoma (BA), <0.33 under-expressed in BA)

Affy ID	Gene Name	Fold Change	P-value
44770_s_at	Cluster Incl. AI341166:qx89h02.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2009715 /clone_end=3' /gb=AI341166 /gi=4078093 /ug=Hs.233977 /len=257'	4.699694547	0.000442
52019_at	Cluster Incl. AI557210:PT2.1_14_H10.r Homo sapiens cDNA, 3 end /clone_end=3' /gb=AI557210 /gi=4489573 /ug=Hs.41271 /len=867'	4.685097403	0.00302
53781_at	Cluster Incl. W74476:zd75a11.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-346460 /clone_end=3' /gb=W74476 /gi=1384763 /ug=Hs.12680 /len=675'	4.663360742	0.003285
56172_at	Cluster Incl. AI979261:wr72g05.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2493272 /clone_end=3' /gb=AI979261 /gi=5804280 /ug=Hs.102720 /len=809'	4.605593005	0.001197
52117_at	Cluster Incl. AI670876:wa06c12.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2297302 /clone_end=3' /gb=AI670876 /gi=4850607 /ug=Hs.44276 /len=798'	4.577288892	0.013189
59614_g_a	Cluster Incl. AI669308:wb85b10.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2312443 /clone_end=3' /gb=AI669308 /gi=4834082 /ug=Hs.196337 /len=632'	4.508059219	0.001927
56688_at	Cluster Incl. AI631355:tz83d05.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2295177 /clone_end=3' /gb=AI631355 /gi=4682685 /ug=Hs.92096 /len=390'	4.461870453	0.001025
59709_at	Cluster Incl. AI675453:wb99f04.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2313823 /clone_end=3' /gb=AI675453 /gi=4875933 /ug=Hs.21432 /len=562'	4.443984215	0.004424
43963_at	Cluster Incl. AI703454:we24d09.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2342033 /clone_end=3' /gb=AI703454 /gi=4991354 /ug=Hs.26176 /len=567'	4.381967582	0.004589
56534_at	Cluster Incl. N20945:yx54f12.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-265583 /clone_end=3' /gb=N20945 /gi=1126115 /ug=Hs.12210 /len=621'	4.354613332	0.000004
49162_f_at	Cluster Incl. AI610692:tp40f03.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2190269 /clone_end=3' /gb=AI610692 /gi=4619859 /ug=Hs.234412 /len=474'	4.340360862	0.00009
54850_at	Cluster Incl. AI860751:w05b07.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2423989 /clone_end=3' /gb=AI860751 /gi=5514367 /ug=Hs.182476 /len=637'	4.319799905	0.004106
51244_at	Cluster Incl. AA447232:zw93a05.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-784496 /clone_end=5' /gb=AA447232 /gi=2159897 /ug=Hs.34806 /len=580'	4.254851949	0.008281
47548_f_at	Cluster Incl. AA621124:af34f07.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1033573 /clone_end=3' /gb=AA621124 /gi=2525063 /ug=Hs.93135 /len=639'	4.238866373	0.00289

Table 3. U95_B Fold Change Genes (>3 over-expressed in Barrett's associated esophageal adenocarcinoma (BA), <0.33 under-expressed in BA)

Affy ID	Gene Name	Fold Change	P-value
42988_at	Cluster Incl. AI344312:tc03e01.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2062776 /clone_end=3' /gb=AI344312 /gi=4081518 /ug=Hs.22011 /len=578'	4.225234676	0.001321
48431_at	Cluster Incl. AI970292:wr09b06.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2481011 /clone_end=3' /gb=AI970292 /gi=5767118 /ug=Hs.20279 /len=605'	4.223781701	0.000002
48077_at	Cluster Incl. AI741321:wg20c02.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2365634 /clone_end=3' /gb=AI741321 /gi=5109609 /ug=Hs.10760 /len=525'	4.208264213	0.000188
44112_at	Cluster Incl. AA224245:zr14h04.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-648823 /clone_end=3' /gb=AA224245 /gi=1844770 /ug=Hs.26612 /len=455'	4.200119211	0.000005
45874_at	Cluster Incl. AI961994:wt41c03.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2510020 /clone_end=3' /gb=AI961994 /gi=5754696 /ug=Hs.30899 /len=433'	4.191359471	0.011876
52275_s_at	Cluster Incl. H11652:ym17g07.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-48178 /clone_end=3' /gb=H11652 /gi=876472 /ug=Hs.236698 /len=481'	4.123364243	0.000508
55755_at	Cluster Incl. AI345945:qp47e12.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1926190 /clone_end=3' /gb=AI345945 /gi=4083151 /ug=Hs.10114 /len=796'	4.108035965	0.000005
48854_i_at	Cluster Incl. AW025683:wu07a09.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2516248 /clone_end=3' /gb=AW025683 /gi=5879213 /ug=Hs.237383 /len=319'	4.071776301	0.000025
53484_at	Cluster Incl. AI631585:wa99g06.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2304346 /clone_end=3' /gb=AI631585 /gi=4682915 /ug=Hs.33977 /len=503'	3.999414942	0.004362
57597_at	Cluster Incl. AW025904:ww71e11.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-991071 /clone_end=3' /gb=AW025904 /gi=5879434 /ug=Hs.123661 /len=674'	3.946689721	0.000247
56940_g_a	Cluster Incl. AI963304:wf61d01.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2511937 /clone_end=3' /gb=AI963304 /gi=5756017 /ug=Hs.110373 /len=660'	3.934211473	0.037291
45144_at	Cluster Incl. AA641636:nr80c04.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1174278 /clone_end=3' /gb=AA641636 /gi=2566854 /ug=Hs.37477 /len=569'	3.920750642	0.008126
55636_at	Cluster Incl. W84893:zd88d09.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-347729 /clone_end=3' /gb=W84893 /gi=1395457 /ug=Hs.9305 /len=619'	3.91767742	0.001305
52349_s_at	Cluster Incl. AA765843:oa25e09.s1 Homo sapiens cDNA /clone=IMAGE-1306024 /gb=AA765843 /gi=2817081 /ug=Hs.238961 /len=496'	3.908250964	0.000084

Table 3. U95_B Fold Change Genes (>3 over-expressed in Barrett's associated esophageal adenocarcinoma (BA), <0.33 under-expressed in BA)

Affy ID	Gene Name	Fold Change	P-value
44744_at	Cluster Incl. A1816843:wj34g08.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2404766 /clone_end=3' /gb=A1816843 /gi=5435922 /ug=Hs.172613 /len=822'	3.885817076	0.00012
45718_at	Cluster Incl. AA426499:zw02b06.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-768083 /clone_end=5' /gb=AA426499 /gi=2106744 /ug=Hs.239900 /len=553'	3.844537888	0.001962
47598_at	Cluster Incl. A1767291:wh25h08.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2381823 /clone_end=3' /gb=A1767291 /gi=5233888 /ug=Hs.97101 /len=601'	3.797287151	0.004107
48546_s_at	Cluster Incl. N30008:yx82e08.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-268262 /clone_end=3' /gb=N30008 /gi=1148528 /ug=Hs.17756 /len=592'	3.759130275	0.000038
51222_at	Cluster Incl. AW007811:wt03d11.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2506389 /clone_end=3' /gb=AW007811 /gi=5856589 /ug=Hs.32793 /len=550'	3.758109572	0.004507
52641_at	Cluster Incl. A1828579:wl42e03.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2427580 /clone_end=3' /gb=A1828579 /gi=5449250 /ug=Hs.239275 /len=384'	3.75632061	0.001209
52337_g_a	Cluster Incl. A1762208:wl54c10.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2394066 /clone_end=3' /gb=A1762208 /gi=5177875 /ug=Hs.238411 /len=553'	3.709836573	0.000216
52290_g_a	Cluster Incl. AA514342:nf56d01.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-923905 /clone_end=3' /gb=AA514342 /gi=2253850 /ug=Hs.236950 /len=606'	3.658373973	0.001941
45331_at	Cluster Incl. AA102468:zm26a12.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-526750 /clone_end=3' /gb=AA102468 /gi=1647486 /ug=Hs.234977 /len=573'	3.627638605	0.00039
52823_at	Cluster Incl. A1620209:tu54d10.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2254867 /clone_end=3' /gb=A1620209 /gi=4629335 /ug=Hs.37916 /len=576'	3.626992495	0.001038
47534_at	Cluster Incl. A1569980:tr90f02.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2226363 /clone_end=3' /gb=A1569980 /gi=4533354 /ug=Hs.9238 /len=495'	3.623794274	0.001497
56223_at	Cluster Incl. A1769689:wj25f12.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2403887 /clone_end=3' /gb=A1769689 /gi=5236198 /ug=Hs.192878 /len=552'	3.617285719	0.00013
56673_at	Cluster Incl. AA769578:nz42a04.s1 Homo sapiens cDNA /clone=IMAGE-1290414 /gb=AA769578 /gi=2820816 /ug=Hs.90488 /len=575	3.598876589	0.001823
48054_at	Cluster Incl. AA024984:ze80c07.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-365292 /clone_end=3' /gb=AA024984 /gi=1489889 /ug=Hs.10574 /len=474'	3.583829556	0.004289

Table 3. U95_B Fold Change Genes (>3 over-expressed in Barrett's associated esophageal adenocarcinoma (BA), <0.33 under-expressed in BA)

Affy ID	Gene Name	Fold Change	P-value
58322_at	Cluster Incl. A1765890:wh66g10.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2385762 /clone_end=3' /gb=A1765890 /gi=5232399 /ug=Hs.16341 /len=511'	3.5683257	0.000325
52826_at	Cluster Incl. AL037412:DKFZp564L0571.s1 Homo sapiens cDNA, 3 end /clone=DKFZp564L0571 /clone_end=3' /gb=AL037412 /gi=5406808 /ug=Hs.38039 /len=804'	3.568196085	0.000189
57195_at	Cluster Incl. A1935271:wp16c05.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2465000 /clone_end=3' /gb=A1935271 /gi=5674141 /ug=Hs.5663 /len=562'	3.544558558	0.000007
44040_at	Cluster Incl. AA524093:ng33f04.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-936607 /clone_end=3' /gb=AA524093 /gi=2265021 /ug=Hs.23158 /len=718'	3.544444641	0.002777
48099_at	Cluster Incl. AA005023:zh96a11.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-429116 /clone_end=3' /gb=AA005023 /gi=1448864 /ug=Hs.10888 /len=593'	3.528226654	0.012069
51270_at	Cluster Incl. AA005361:zh97b01.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-429193 /clone_end=3' /gb=AA005361 /gi=1448394 /ug=Hs.36723 /len=690'	3.504429429	0.00292
49888_f at	Cluster Incl. A1357616:qu20g08.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1965374 /clone_end=3' /gb=A1357616 /gi=4109237 /ug=Hs.101651 /len=405'	3.47870117	0.000114
51160_at	Cluster Incl. AA004208:zh97c02.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-429218 /clone_end=3' /gb=AA004208 /gi=1448403 /ug=Hs.27437 /len=665'	3.477061385	0.000445
45826_at	Cluster Incl. AA044844 /gi=1523066 /ug=Hs.5944 /len=645'	3.434292964	0.000168
52016_at	Cluster Incl. A1672414:ty64h06.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2283899 /clone_end=3' /gb=A1672414 /gi=4852145 /ug=Hs.41241 /len=536'	3.423366376	0.001144
46720_at	Cluster Incl. A1066598:ov47g09.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1640512 /clone_end=3' /gb=A1066598 /gi=3367300 /ug=Hs.9853 /len=760'	3.418349709	0.000205
48545_at	Cluster Incl. W87383:zh66f09.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-417065 /clone_end=5' /gb=W87383 /gi=1401438 /ug=Hs.17731 /len=625'	3.403794238	0.000121
44630_at	Cluster Incl. AA521049:aa71c10.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-826386 /clone_end=3' /gb=AA521049 /gi=2261592 /ug=Hs.34487 /len=593'	3.356102325	0.003255
54625_at	Cluster Incl. AA057543:zl93d01.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-512161 /clone_end=3' /gb=AA057543 /gi=1550248 /ug=Hs.15911 /len=655'	3.35563894	0.003164

Table 3. U95_B Fold Change Genes (>3 over-expressed in Barrett's associated esophageal adenocarcinoma (BA), <0.33 under-expressed in BA)

Affy ID	Gene Name	Fold Change	P-value
42831_at	Cluster Incl. AI201843:qs76f10.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1944043 /clone_end=3' /gb=AI201843 /gi=3754449 /ug=Hs.169133 /len=358'	3.352230883	0.000686
44778_g_a	Cluster Incl. AA553396:nk80b05.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1019793 /clone_end=3' /gb=AA553396 /gi=2323935 /ug=Hs.234190 /len=454'	3.349340084	0.001436
48540_at	Cluster Incl. R26843:yh52a03.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-133324 /clone_end=3' /gb=R26843 /gi=782978 /ug=Hs.17558 /len=490'	3.348102248	0.006734
55752_at	Cluster Incl. AI198880:qf66c09.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1754992 /clone_end=3' /gb=AI198880 /gi=3751486 /ug=Hs.10098 /len=786'	3.344024791	0.004837
57171_at	Cluster Incl. X84716:HSEST92 Homo sapiens cDNA /clone=MEC-92 /gb=X84716 /gi=673403 /ug=Hs.29748 /len=1214	3.338417032	0.000053
48013_at	Cluster Incl. AI768116:wg81c10.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2371506 /clone_end=3' /gb=AI768116 /gi=5234625 /ug=Hs.10086 /len=557'	3.322252213	0.015046
51840_at	Cluster Incl. AI765436:wi80a08.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2399606 /clone_end=3' /gb=AI765436 /gi=5231945 /ug=Hs.5605 /len=498'	3.318140109	0.020706
45228_at	Cluster Incl. AI271425:qi19b04.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1856911 /clone_end=3' /gb=AI271425 /gi=3890592 /ug=Hs.43749 /len=551'	3.317124397	0.007521
52062_f_at	Cluster Incl. H98105:yx09b10.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-261211 /clone_end=3' /gb=H98105 /gi=1118990 /ug=Hs.42491 /len=584'	3.313066937	0.002819
50795_at	Cluster Incl. AI693592:wd79a05.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2337776 /clone_end=3' /gb=AI693592 /gi=4970932 /ug=Hs.112712 /len=508'	3.31259622	0.000537
57022_at	Cluster Incl. AI742490:wg43e10.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2367882 /clone_end=3' /gb=AI742490 /gi=5110778 /ug=Hs.112885 /len=550'	3.310509474	0.000572
42999_at	Cluster Incl. AI758408:ty68f09.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2284265 /clone_end=3' /gb=AI758408 /gi=5152131 /ug=Hs.22247 /len=633'	3.305590563	0.007574
58695_at	Cluster Incl. AA461376:zx70g03.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-796852 /clone_end=5' /gb=AA461376 /gi=2186496 /ug=Hs.9625 /len=588'	3.290571553	0.000149
47110_at	Cluster Incl. AA205598:zq68d01.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-646753 /clone_end=3' /gb=AA205598 /gi=1803606 /ug=Hs.86366 /len=618'	3.286952373	0.011612

Table 3. U95_B Fold Change Genes (>3 over-expressed in Barrett's associated esophageal adenocarcinoma (BA), <0.33 under-expressed in BA)

Affy ID	Gene Name	Fold Change	P-value
53922_at	Cluster Incl. AA195789:zp95b07.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-627925 /clone_end=5' /gb=AA195789 /gi=1791380 /ug=Hs.60440 /len=619'	3.282601218	0.015234
47899_at	Cluster Incl. AA056755:zk81g02.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-489266 /clone_end=3' /gb=AA056755 /gi=1549130 /ug=Hs.151714 /len=496'	3.276090147	0.007052
43053_g_a	Cluster Incl. AW025012:wu93a04.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-990913 /clone_end=3' /gb=AW025012 /gi=5878542 /ug=Hs.23295 /len=520'	3.25557678	0.00068
48080_at	Cluster Incl. AI566481:tr60d03.x2 Homo sapiens cDNA, 3 end /clone=IMAGE-2222693 /clone_end=3' /gb=AI566481 /gi=4524933 /ug=Hs.10784 /len=551'	3.224686597	0.000089
50417_at	Cluster Incl. AA641023:nr72c02.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1173506 /clone_end=3' /gb=AA641023 /gi=2566273 /ug=Hs.25303 /len=571'	3.222451104	0.000231
55749_at	Cluster Incl. AA135720:zl11b08.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-501591 /clone_end=3' /gb=AA135720 /gi=1696732 /ug=Hs.10083 /len=563'	3.211891299	0.002311
45390_at	Cluster Incl. AI769269:wg35h12.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2367143 /clone_end=3' /gb=AI769269 /gi=5235778 /ug=Hs.239541 /len=443'	3.203408013	0.001334
56035_at	Cluster Incl. AL041162:DKFZp434G1516.s1 Homo sapiens cDNA, 3 end /clone=DKFZp434G1516 /clone_end=3' /gb=AL041162 /gi=5410098 /ug=Hs.98587 /len=775'	3.199890488	0.000887
54594_at	Cluster Incl. AA009571:zi04h05.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-429849 /clone_end=5' /gb=AA009571 /gi=1470709 /ug=Hs.82290 /len=467'	3.199200539	0.042469
56827_at	Cluster Incl. AI932306:wd26g11.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2329316 /clone_end=3' /gb=AI932306 /gi=5671043 /ug=Hs.105463 /len=528'	3.177892231	0.000647
45143_at	Cluster Incl. AA160973:zq40h10.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-632227 /clone_end=3' /gb=AA160973 /gi=1735680 /ug=Hs.37443 /len=544'	3.169675904	0.000021
44974_at	Cluster Incl. AI970896:wr21b11.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2488317 /clone_end=3' /gb=AI970896 /gi=5767722 /ug=Hs.233634 /len=514'	3.140815237	0.001848
54049_at	Cluster Incl. AI652991:wb42b11.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2308317 /clone_end=3' /gb=AI652991 /gi=4736970 /ug=Hs.6682 /len=528'	3.138854596	0.014071
59346_at	Cluster Incl. W96205:ze10d04.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-358567 /clone_end=3' /gb=W96205 /gi=1426131 /ug=Hs.163703 /len=408'	3.133106727	0.018285

Table 3. U95_B Fold Change Genes (>3 over-expressed in Barrett's associated esophageal adenocarcinoma (BA), <0.33 under-expressed in BA)

Affy ID	Gene Name	Fold Change	P-value
45280_at	Cluster Incl. AA703316:zj11b07.s1 Homo sapiens cDNA, 3 end /clone=449941 /clone_end=3' /gb=AA703316 /gi=2713234 /ug=Hs.19221 /len=499'	3.093960419	0.000016
50287_at	Cluster Incl. R61210:yh06e09.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-42341 /clone_end=5' /gb=R61210 /gi=831905 /ug=Hs.239431 /len=551'	3.083985493	0.023892
58317_at	Cluster Incl. A1638611:tt31b11.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2242365 /clone_end=3' /gb=A1638611 /gi=4690845 /ug=Hs.16229 /len=639'	3.068722453	0.000172
51155_at	Cluster Incl. AL043669:DKFZp434J2027_s1 Homo sapiens cDNA, 3 end /clone=DKFZp434J2027 /clone_end=3' /gb=AL043669 /gi=5423056 /ug=Hs.27268 /len=540'	3.056662545	0.002265
43366_at	Cluster Incl. A1979079:wr70b09.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2493017 /clone_end=3' /gb=A1979079 /gi=5804109 /ug=Hs.233723 /len=490'	3.055354669	0.007779
52848_at	Cluster Incl. A1491983:to07e03.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2178364 /clone_end=3' /gb=A1491983 /gi=4392986 /ug=Hs.74911 /len=655'	3.008324353	0.003676
57596_at	Cluster Incl. T75313:yc89d05.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-23443 /clone_end=5' /gb=T75313 /gi=692075 /ug=Hs.12365 /len=530'	3.001649666	0.020524
43994_at	Cluster Incl. A1333224:qq05h01.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1931665 /clone_end=3' /gb=A1333224 /gi=4069783 /ug=Hs.26955 /len=504'	3.000320561	0.004173
43993_at	Cluster Incl. AA223148:zr07g09.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-650848 /clone_end=3' /gb=AA223148 /gi=1843707 /ug=Hs.26942 /len=492'	0.328758769	0.000839
42833_g_a	Cluster Incl. W61185:zd31c11.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-342260 /clone_end=3' /gb=W61185 /gi=1368020 /ug=Hs.169345 /len=400'	0.328541123	0.000416
45878_at	Cluster Incl. W21966:59c7 Homo sapiens cDNA /clone=(not-directional) /gb=W21966 /gi=1298799 /ug=Hs.31097 /len=767	0.328253841	0.000258
44711_at	Cluster Incl. A1928869:au64d01.x1 Homo sapiens cDNA /clone=IMAGE /gb=A1928869 /gi=5664768 /ug=Hs.15977 /len=630	0.327580662	0.023675
50314_i_at	Cluster Incl. A1761506:w161b11.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2394717 /clone_end=3' /gb=A1761506 /gi=5177173 /ug=Hs.239692 /len=544'	0.326479347	0.018768
42065_at	Cluster Incl. H28581:y163e11.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-162956 /clone_end=3' /gb=H28581 /gi=898934 /ug=Hs.92711 /len=416'	0.324964383	0.000041

Table 3. U95_B Fold Change Genes (>3 over-expressed in Barrett's associated esophageal adenocarcinoma (BA), <0.33 under-expressed in BA)

Affy ID	Gene Name	Fold Change	P-value
46079_at	Cluster Incl. W63785:zd30g09.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-342208 /clone_end=3' /gb=W63785 /gi=1371386 /ug=Hs.57843 /len=495'	0.319996048	0.000015
42987_at	Cluster Incl. AI003579:ai88d07.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1387885 /clone_end=3' /gb=AI003579 /gi=3203913 /ug=Hs.22003 /len=600'	0.318539582	0.000912
57915_at	Cluster Incl. AA613523:nq22d01.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1144609 /clone_end=3' /gb=AA613523 /gi=2464561 /ug=Hs.22824 /len=507'	0.315418617	0.001639
56272_at	Cluster Incl. AI827230:w109e02.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2424410 /clone_end=3' /gb=AI827230 /gi=5447901 /ug=Hs.20665 /len=748'	0.311014472	0.001289
59466_at	Cluster Incl. AA447295:AC.F02R Homo sapiens cDNA, 5 end /clone=AC.F02 /clone_end=5' /gb=AA447295 /gi=3025381 /ug=Hs.168953 /len=589'	0.310739955	0.002774
42803_at	Cluster Incl. AI377305:te60a03.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2091052 /clone_end=3' /gb=AI377305 /gi=4187158 /ug=Hs.165694 /len=474'	0.307373662	0.00498
46200_at	Cluster Incl. AA742697:mx30g04.s1 Homo sapiens cDNA /clone=IMAGE-1257654 /gb=AA742697 /gi=2782203 /ug=Hs.62492 /len=526	0.307203732	0.04226
45635_at	Cluster Incl. AI801898:tx28h03.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2270933 /clone_end=3' /gb=AI801898 /gi=5367370 /ug=Hs.47166 /len=604'	0.306826026	0.001547
46095_at	Cluster Incl. AL044632:DKFZp434O082_r1 Homo sapiens cDNA, 5 end /clone=DKFZp434O082 /clone_end=5' /gb=AL044632 /gi=5432847 /ug=Hs.55016 /len=554'	0.306352205	0.003349
47653_r at	Cluster Incl. AW023468:df55c11.y1 Homo sapiens cDNA, 5 end /clone=IMAGE-2487188 /clone_end=5' /gb=AW023468 /gi=5876998 /ug=Hs.165320 /len=473'	0.306297842	0.003547
43046_at	Cluster Incl. AI419030:ff53b01.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2102953 /clone_end=3' /gb=AI419030 /gi=4264961 /ug=Hs.23202 /len=473'	0.306182917	0.034114
49227_at	Cluster Incl. H09620:y97f09.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-46287 /clone_end=3' /gb=H09620 /gi=874442 /ug=Hs.23783 /len=531'	0.303321471	0.001357
52988_at	Cluster Incl. AI765981:wj23a06.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2403634 /clone_end=3' /gb=AI765981 /gi=5232490 /ug=Hs.49657 /len=580'	0.303206128	0.000057
58356_at	Cluster Incl. AA142978:z149d03.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-505253 /clone_end=3' /gb=AA142978 /gi=1712437 /ug=Hs.167951 /len=654'	0.301800249	0.000424

Table 3. U95_B Fold Change Genes (>3 over-expressed in Barrett's associated esophageal adenocarcinoma (BA), <0.33 under-expressed in BA)

Affy ID	Gene Name	Fold Change	P-value
53275_at	Cluster Incl. AA829709:oe50e07.s1 Homo sapiens cDNA /clone=IMAGE-1415076 /gb=AA829709 /gi=2902808 /ug=Hs.28733 /len=438	0.301386846	0.00009
55107_at	Cluster Incl. AI916306:we29c09.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2342512 /clone_end=3' /gb=AI916306 /gi=5636251 /ug=Hs.87125 /len=532'	0.300526553	0.000003
42909_at	Cluster Incl. AA281967:zt11g07.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-712860 /clone_end=3' /gb=AA281967 /gi=1924791 /ug=Hs.221168 /len=454'	0.299343167	0.000852
42832_at	Cluster Incl. W61185:zd31c11.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-342260 /clone_end=3' /gb=W61185 /gi=1368020 /ug=Hs.169345 /len=400'	0.298246963	0.000023
44599_at	Cluster Incl. AA631908:np78a09.s1 Homo sapiens cDNA /clone=IMAGE-1132408 /gb=AA631908 /gi=2554519 /ug=Hs.32417 /len=569	0.2973351	0.000806
46169_at	Cluster Incl. AI745624:wc33h03.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2317013 /clone_end=3' /gb=AI745624 /gi=5113912 /ug=Hs.6065 /len=574'	0.297165449	0.00003
43063_at	Cluster Incl. AA584408:nn81b03.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1090253 /clone_end=3' /gb=AA584408 /gi=2369017 /ug=Hs.233852 /len=620'	0.296993211	0.009651
54831_r_at	Cluster Incl. AA147881:zl50a04.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-505326 /clone_end=3' /gb=AA147881 /gi=1717297 /ug=Hs.180777 /len=620'	0.295444255	0.000453
50411_at	Cluster Incl. AI659533:tu12a12.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2250814 /clone_end=3' /gb=AI659533 /gi=4763103 /ug=Hs.25248 /len=654'	0.294474802	0.008774
46628_at	Cluster Incl. AI636631:ts92a04.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2238702 /clone_end=3' /gb=AI636631 /gi=4687961 /ug=Hs.6828 /len=495'	0.293823752	0.003684
56238_at	Cluster Incl. AI589776:tm74c04.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2163846 /clone_end=3' /gb=AI589776 /gi=4598824 /ug=Hs.19447 /len=760'	0.293416233	0.004513
47283_at	Cluster Incl. AA398628:zl74e03.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-728092 /clone_end=3' /gb=AA398628 /gi=2051737 /ug=Hs.163845 /len=467'	0.293232708	0.00032
57143_r_at	Cluster Incl. AI740811:wg24e02.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2366042 /clone_end=3' /gb=AI740811 /gi=5109099 /ug=Hs.23579 /len=572'	0.292284773	0.002541
58104_at	Cluster Incl. AI161427:qc78f03.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1715741 /clone_end=3' /gb=AI161427 /gi=3693188 /ug=Hs.104871 /len=436'	0.291974611	0.000569

Table 3. U95_B Fold Change Genes (>3 over-expressed in Barrett's associated esophageal adenocarcinoma (BA), <0.33 under-expressed in BA)

Affy ID	Gene Name	Fold Change	P-value
44680_at	Cluster Incl. AA464020:zx86a03.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-810604 /clone_end=5' /gb=AA464020 /gi=2188904 /ug=Hs.32246 /len=534'	0.291478075	0.000129
58015_at	Cluster Incl. AA93222:ou02c09.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1625104 /clone_end=3' /gb=AA93222 /gi=3179767 /ug=Hs.101915 /len=471'	0.290171632	0.000436
47918_at	Cluster Incl. H17938:ym37a06.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-50084 /clone_end=3' /gb=H17938 /gi=884178 /ug=Hs.16365 /len=473'	0.289844258	0.000045
44031_at	Cluster Incl. A1478812:tm52f03.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2161757 /clone_end=3' /gb=A1478812 /gi=4373625 /ug=Hs.28917 /len=511'	0.289231972	0.000021
45260_at	Cluster Incl. W22565:70E5 Homo sapiens cDNA /clone=(not-directional) /gb=W22565 /gi=1299447 /ug=Hs.182344 /len=805	0.288048543	0.010503
50190_at	Cluster Incl. A1697875:we18c06.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2341450 /clone_end=3' /gb=A1697875 /gi=4985775 /ug=Hs.31664 /len=551'	0.28704917	0.00027
52125_at	Cluster Incl. A1991041:wu36b09.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-990828 /clone_end=3' /gb=A1991041 /gi=5837938 /ug=Hs.44579 /len=534'	0.28697383	0.001537
52480_at	Cluster Incl. A1334409:qq26b07.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1933621 /clone_end=3' /gb=A1334409 /gi=4070968 /ug=Hs.26192 /len=439'	0.286020382	0.002088
43601_g_a	Cluster Incl. AA100793:zm26c02.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-526754 /clone_end=3' /gb=AA100793 /gi=1647210 /ug=Hs.193380 /len=500'	0.285572376	0.017485
42242_at	Cluster Incl. AA978128:op32e03.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1578556 /clone_end=3' /gb=AA978128 /gi=3155574 /ug=Hs.99513 /len=382'	0.284819299	0.000022
44256_g_a	Cluster Incl. AA480017:zv18e06.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-754018 /clone_end=5' /gb=AA480017 /gi=2208168 /ug=Hs.226513 /len=499'	0.284758761	0.037516
49125_at	Cluster Incl. A1609604:tw91e09.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2267080 /clone_end=3' /gb=A1609604 /gi=4618771 /ug=Hs.227806 /len=460'	0.284325628	0.015787
49819_at	Cluster Incl. A1432375:tg54h06.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2112635 /clone_end=3' /gb=A1432375 /gi=4281193 /ug=Hs.99083 /len=470'	0.283787158	0.000007
53914_at	Cluster Incl. A1767222:wi94e09.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2401000 /clone_end=3' /gb=A1767222 /gi=5233731 /ug=Hs.15830 /len=651'	0.283775141	0.000275

Table 3. U95_B Fold Change Genes (>3 over-expressed in Barrett's associated esophageal adenocarcinoma (BA), <0.33 under-expressed in BA)

Affy ID	Gene Name	Fold Change	P-value
47324_at	Cluster Incl. AA199881:zq52f10.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-645259 /clone_end=3' /gb=AA199881 /gi=1795588 /ug=Hs.58350 /len=511'	0.283572718	0
53796_at	Cluster Incl. AI819282:wj05f11.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2401965 /clone_end=3' /gb=AI819282 /gi=5438361 /ug=Hs.12936 /len=593'	0.283060388	0.04394
47481_at	Cluster Incl. AA621478:af92e12.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1055278 /clone_end=3' /gb=AA621478 /gi=2525417 /ug=Hs.130699 /len=398'	0.282636217	0.016871
45333_at	Cluster Incl. AI525592:PT1.3_03_F03.r Homo sapiens cDNA, 5 end /clone_end=5' /gb=AI525592 /gi=4439727 /ug=Hs.23579 /len=887'	0.279658196	0.000052
59126_at	Cluster Incl. AI660548:we68a05.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2346224 /clone_end=3' /gb=AI660548 /gi=4764118 /ug=Hs.19165 /len=501'	0.278719933	0.0035
48822_s_at	Cluster Incl. AW015546:UI-H-B10p-aau-d-11-O-UI.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-2710700 /clone_end=3' /gb=AW015546 /gi=5864303 /ug=Hs.234250 /len=629'	0.27784195	0.004766
43395_s_at	Cluster Incl. AW006148:wz92h09.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2566337 /clone_end=3' /gb=AW006148 /gi=5854926 /ug=Hs.234072 /len=502'	0.277596215	0.030595
47071_at	Cluster Incl. AI279709:ql53e09.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1876072 /clone_end=3' /gb=AI279709 /gi=3917943 /ug=Hs.79741 /len=601'	0.276885721	0
58454_at	Cluster Incl. AI738919:wi12a04.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2389998 /clone_end=3' /gb=AI738919 /gi=5100900 /ug=Hs.239355 /len=648'	0.274374246	0.000036
54369_at	Cluster Incl. AI242381:qi15f07.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1856581 /clone_end=3' /gb=AI242381 /gi=3837778 /ug=Hs.47282 /len=263'	0.274129957	0.000022
54310_at	Cluster Incl. AA975511:on30e03.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1558204 /clone_end=3' /gb=AA975511 /gi=3151303 /ug=Hs.44565 /len=497'	0.272632887	0.003
50151_at	Cluster Incl. AA403227:zv68h05.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-758649 /clone_end=5' /gb=AA403227 /gi=2055725 /ug=Hs.29604 /len=557'	0.271893984	0.000269
46011_at	Cluster Incl. AI916225:wi49f07.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2393605 /clone_end=3' /gb=AI916225 /gi=5636080 /ug=Hs.58559 /len=507'	0.269822445	0.000412
56216_at	Cluster Incl. AA740543:ob28g10.s1 Homo sapiens cDNA /clone=IMAGE-1325058 /gb=AA740543 /gi=2779135 /ug=Hs.103913 /len=486	0.269334271	0.001353

Table 3. U95_B Fold Change Genes (>3 over-expressed in Barrett's associated esophageal adenocarcinoma (BA), <0.33 under-expressed in BA)

Affy ID	Gene Name	Fold Change	P-value
57452_at	Cluster Incl. AA451798:zx46b07.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-795253 /clone_end=5' /gb=AA451798 /gi=2165467 /ug=Hs.99249 /len=407'	0.268116773	0.000009
45456_at	Cluster Incl. R60584:yh14g05.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-37856 /clone_end=3' /gb=R60584 /gi=831279 /ug=Hs.26789 /len=492'	0.26781965	0.007247
46105_at	Cluster Incl. AA149641:zi39c08.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-504302 /clone_end=3' /gb=AA149641 /gi=1720442 /ug=Hs.55405 /len=570'	0.267205089	0.000264
58567_s at	Cluster Incl. AI308197:tb25g11.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2055428 /clone_end=3' /gb=AI308197 /gi=4002832 /ug=Hs.40496 /len=462'	0.265573576	0.034363
58359_g a	Cluster Incl. AA142978:zi49d03.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-505253 /clone_end=3' /gb=AA142978 /gi=1712437 /ug=Hs.167951 /len=654'	0.264528974	0.000057
53166_at	Cluster Incl. W74591:zd77g09.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-346720 /clone_end=3' /gb=W74591 /gi=1384892 /ug=Hs.5771 /len=663'	0.263493949	0.002128
45256_at	Cluster Incl. AI271460:qi19e06.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1856962 /clone_end=3' /gb=AI271460 /gi=3890627 /ug=Hs.181368 /len=559'	0.259328936	0.001801
47771_at	Cluster Incl. AA234670:zs37f06.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-687395 /clone_end=5' /gb=AA234670 /gi=1859377 /ug=Hs.62654 /len=316'	0.257739498	0.000014
59704_at	Cluster Incl. H15288:ym30g12.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-49810 /clone_end=3' /gb=H15288 /gi=880108 /ug=Hs.21420 /len=562'	0.256002125	0.000103
48896_at	Cluster Incl. AI082244:ox79g07.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1662588 /clone_end=3' /gb=AI082244 /gi=3419036 /ug=Hs.93764 /len=552'	0.255967313	0.000028
45210_at	Cluster Incl. AA035736:ze25b11.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-359997 /clone_end=5' /gb=AA035736 /gi=1507626 /ug=Hs.4285 /len=470'	0.255599052	0.000002
AFFX-HUM	M33197 Human glyceraldehyde-3-phosphate dehydrogenase (GAPDH) mRNA, complete cds (5, M, 3 represent transcript regions 5 prime, Middle, and 3 prime respectively)	0.253971231	0.02209
50223_at	Cluster Incl. AA020743:ze63c11.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-363668 /clone_end=3' /gb=AA020743 /gi=1484525 /ug=Hs.234026 /len=626'	0.2536657497	0.048419
47097_at	Cluster Incl. AI674565:wc03c02.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2314082 /clone_end=3' /gb=AI674565 /gi=4875045 /ug=Hs.8379 /len=563'	0.252742984	0.000395

Table 3. U95_B Fold Change Genes (>3 over-expressed in Barrett's associated esophageal adenocarcinoma (BA), <0.33 under-expressed in BA)

Affy ID	Gene Name	Fold Change	P-value
50361_at	Cluster Incl. A1658662:tu22a11.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2251772 /clone_end=3' /gb=A1658662 /gi=4762232 /ug=Hs.24192 /len=503'	0.247649714	0.007879
58288_at	Cluster Incl. W63676:zd30b03.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-342125 /clone_end=3' /gb=W63676 /gi=1371257 /ug=Hs.15641 /len=627'	0.246615101	0.000134
57772_g_a	Cluster Incl. AA886870:oj25g11.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1493252 /clone_end=3' /gb=AA886870 /gi=3001978 /ug=Hs.107381 /len=572'	0.246598396	0.00327
41955_r_at	Cluster Incl. Z41561:HSCZYA022 Homo sapiens cDNA, 3 end /clone=c-zya02 /clone_end=3' /gb=Z41561 /gi=567709 /ug=Hs.65739 /len=251'	0.244644274	0.000008
57141_f_at	Cluster Incl. A1740811:wg24e02.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2366042 /clone_end=3' /gb=A1740811 /gi=5109099 /ug=Hs.23579 /len=572'	0.244451584	0.000034
55525_at	Cluster Incl. A1972498:wr38c04.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2489958 /clone_end=3' /gb=A1972498 /gi=5769244 /ug=Hs.97469 /len=546'	0.240971633	0.00039
47124_at	Cluster Incl. A1672049:ty63b04.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2283727 /clone_end=3' /gb=A1672049 /gi=4851780 /ug=Hs.8734 /len=574'	0.239306276	0.022482
44606_at	Cluster Incl. AA205873:zq54c06.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-645418 /clone_end=3' /gb=AA205873 /gi=1801444 /ug=Hs.32807 /len=528'	0.238440601	0.000031
51909_at	Cluster Incl. A1130027:qc36c08.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1711694 /clone_end=3' /gb=A1130027 /gi=3598541 /ug=Hs.65748 /len=461'	0.236891013	0.007448
46691_at	Cluster Incl. A1472143:ij86b02.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2148363 /clone_end=3' /gb=A1472143 /gi=4334233 /ug=Hs.92198 /len=613'	0.236351122	0.00165
47578_at	Cluster Incl. AA160156:zo81c09.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-593296 /clone_end=3' /gb=AA160156 /gi=1734749 /ug=Hs.95612 /len=528'	0.235200728	0.000029
48476_at	Cluster Incl. A1768887:wh71f02.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2386203 /clone_end=3' /gb=A1768887 /gi=5235396 /ug=Hs.21958 /len=539'	0.23307379	0.000002
49709_at	Cluster Incl. AA127924:zl13h06.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-501851 /clone_end=3' /gb=AA127924 /gi=1687231 /ug=Hs.71034 /len=578'	0.231365733	0.000001
43412_s_at	Cluster Incl. AA622152:nq56e11.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1147916 /clone_end=3' /gb=AA622152 /gi=2526028 /ug=Hs.234262 /len=414'	0.230949759	0.000001

Table 3. U95_B Fold Change Genes (>3 over-expressed in Barrett's associated esophageal adenocarcinoma (BA), <0.33 under-expressed in BA)

Affy ID	Gene Name	Fold Change	P-value
56894_at	Cluster Incl. N29070:yx41d02.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-264291 /clone_end=5' /gb=N29070 /gi=1147306 /ug=Hs.108923 /len=489'	0.229718565	0
46927_at	Cluster Incl. AA086045:z184e03.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-511324 /clone_end=3' /gb=AA086045 /gi=1629586 /ug=Hs.137313 /len=518'	0.229016351	0.000019
47474_at	Cluster Incl. H40296:yn86d03.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-175301 /clone_end=3' /gb=H40296 /gi=916348 /ug=Hs.127588 /len=398'	0.228996683	0.005309
45386_at	Cluster Incl. A1924317:wn55c12.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2449366 /clone_end=3' /gb=A1924317 /gi=5660281 /ug=Hs.239375 /len=490'	0.228351474	0.000023
47650_at	Cluster Incl. AA397625:z179d07.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-728557 /clone_end=5' /gb=AA397625 /gi=2050727 /ug=Hs.163913 /len=429'	0.228224396	0.001661
46476_at	Cluster Incl. AA531287:nj09e04.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-985854 /clone_end=3' /gb=AA531287 /gi=2273993 /ug=Hs.105805 /len=507'	0.226386204	0.004254
48050_at	Cluster Incl. A1817448:wk38e01.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2417688 /clone_end=3' /gb=A1817448 /gi=5436527 /ug=Hs.105421 /len=572'	0.225524389	0.000145
49985_at	Cluster Incl. A1917602:wi35g02.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2392274 /clone_end=3' /gb=A1917602 /gi=5637457 /ug=Hs.106440 /len=530'	0.224810828	0.00025
45747_at	Cluster Incl. AA127810:zk88a10.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-489882 /clone_end=5' /gb=AA127810 /gi=1687089 /ug=Hs.30376 /len=619'	0.218922022	0.001011
52999_at	Cluster Incl. AA126704:z129b10.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-503323 /clone_end=3' /gb=AA126704 /gi=1688008 /ug=Hs.50107 /len=588'	0.215581442	0.007024
46120_at	Cluster Incl. AA149250:z126d06.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-503051 /clone_end=3' /gb=AA149250 /gi=1719966 /ug=Hs.56105 /len=575'	0.215193255	0.03997
47928_at	Cluster Incl. A1858054:wj69g04.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2408118 /clone_end=3' /gb=A1858054 /gi=5511670 /ug=Hs.165169 /len=746'	0.215190727	0.002954
48039_at	Cluster Incl. A1634580:tz30b04.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2290063 /clone_end=3' /gb=A1634580 /gi=4685910 /ug=Hs.10339 /len=686'	0.21474006	0.017632
43600_at	Cluster Incl. AA100793:zm26c02.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-526754 /clone_end=3' /gb=AA100793 /gi=1647210 /ug=Hs.193380 /len=500'	0.211158214	0.001494

Table 3. U95_B Fold Change Genes (>3 over-expressed in Barrett's associated esophageal adenocarcinoma (BA), <0.33 under-expressed in BA)

Affy ID	Gene Name	Fold Change	P-value
46699_at	Cluster Incl. AI052110:oy30a11.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1667324 /clone_end=3' /gb=AI052110 /gi=3308101 /ug=Hs.93961 /len=567'	0.210882988	0.004296
46700_at	Cluster Incl. W55956:zc58g06.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-326554 /clone_end=5' /gb=W55956 /gi=1358060 /ug=Hs.94030 /len=622'	0.210863305	0.004741
53011_at	Cluster Incl. AA036952:zk30h01.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-472081 /clone_end=3' /gb=AA036952 /gi=1510009 /ug=Hs.50841 /len=571'	0.210525571	0.003777
45394_s at	Cluster Incl. AA563933:nk23b02.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1014315 /clone_end=3' /gb=AA563933 /gi=2335572 /ug=Hs.239604 /len=518'	0.209901504	0.003068
46199_at	Cluster Incl. AI076809:oz01a06.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1674034 /clone_end=3' /gb=AI076809 /gi=3404638 /ug=Hs.62472 /len=516'	0.208199399	0.000172
59560_at	Cluster Incl. AI669751:tu12g01.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2250864 /clone_end=3' /gb=AI669751 /gi=4834525 /ug=Hs.175783 /len=692'	0.206207696	0.000002
45207_at	Cluster Incl. N42752:yy11g08.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-270974 /clone_end=5' /gb=N42752 /gi=1167182 /ug=Hs.42645 /len=535'	0.205356842	0.000126
48436_at	Cluster Incl. AI922968:wm66h03.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2450453 /clone_end=3' /gb=AI922968 /gi=5659018 /ug=Hs.203485 /len=498'	0.203844179	0.000015
48421_at	Cluster Incl. AI990027:ws37c08.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2499374 /clone_end=3' /gb=AI990027 /gi=5836908 /ug=Hs.19813 /len=554'	0.201114358	0.000466
47982_at	Cluster Incl. AA630981:nq76c07.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1158252 /clone_end=3' /gb=AA630981 /gi=2553592 /ug=Hs.174024 /len=475'	0.1965858	0.001398
46188_at	Cluster Incl. AI422243:tf58h09.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2103521 /clone_end=3' /gb=AI422243 /gi=4268174 /ug=Hs.61762 /len=593'	0.196273084	0.001778
52080_at	Cluster Incl. AI864898:wj66d08.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2407791 /clone_end=3' /gb=AI864898 /gi=5529005 /ug=Hs.43125 /len=523'	0.194711313	0.003268
47123_at	Cluster Incl. AI247543:qh60c07.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1849068 /clone_end=3' /gb=AI247543 /gi=3842940 /ug=Hs.87310 /len=699'	0.194396588	0.000008
48367_at	Cluster Incl. H62656:yr45a06.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-208210 /clone_end=5' /gb=H62656 /gi=1017002 /ug=Hs.182670 /len=504'	0.193760977	0.000029

Table 3. U95_B Fold Change Genes (>3 over-expressed in Barrett's associated esophageal adenocarcinoma (BA), <0.33 under-expressed in BA)

Affy ID	Gene Name	Fold Change	P-value
43849_s_at	Cluster Incl. AA622570:np21f04.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1116991 /clone_end=3' /gb=AA622570 /gi=2526446 /ug=Hs.238528 /len=461'	0.190479348	0.002324
58902_r_at	Cluster Incl. R44987:yg33g06.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-34444 /clone_end=3' /gb=R44987 /gi=824341 /ug=Hs.124207 /len=481'	0.188238717	0.000376
48981_at	Cluster Incl. AI954620:wq34c02.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2473154 /clone_end=3' /gb=AI954620 /gi=5746930 /ug=Hs.97499 /len=545'	0.188158824	0.000359
47605_at	Cluster Incl. AI022657:ox05h04.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1655479 /clone_end=3' /gb=AI022657 /gi=3237898 /ug=Hs.97345 /len=710'	0.187925204	0.000006
51610_at	Cluster Incl. AI808807:wf97e02.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2363546 /clone_end=3' /gb=AI808807 /gi=5395373 /ug=Hs.17404 /len=538'	0.187409743	0.000242
47329_at	Cluster Incl. AI092869:qa77c01.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1692768 /clone_end=3' /gb=AI092869 /gi=3431845 /ug=Hs.58611 /len=430'	0.186424395	0.000245
50648_at	Cluster Incl. AI763136:wi65a06.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2398162 /clone_end=3' /gb=AI763136 /gi=5178803 /ug=Hs.165215 /len=558'	0.184618742	0
58057_r_at	Cluster Incl. AA009593:ze82f11.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-365517 /clone_end=3' /gb=AA009593 /gi=1470752 /ug=Hs.103296 /len=511'	0.181735047	0.000014
52140_at	Cluster Incl. AL046941:DKFZp586l0717_r1 Homo sapiens cDNA, 5 end /clone=DKFZp586l0717 /clone_end=5' /gb=AL046941 /gi=5435000 /ug=Hs.46531 /len=704'	0.181720222	0.01492
52634_at	Cluster Incl. AW025596:wu75d09.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-990756 /clone_end=3' /gb=AW025596 /gi=5879126 /ug=Hs.238927 /len=488'	0.180172622	0.000001
52742_at	Cluster Incl. AI767756:wh39d09.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2383121 /clone_end=3' /gb=AI767756 /gi=5234265 /ug=Hs.82302 /len=501'	0.179940127	0.000009
51291_at	Cluster Incl. W91952:zh47f03.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-415229 /clone_end=5' /gb=W91952 /gi=1424313 /ug=Hs.37331 /len=594'	0.179194305	0.001469
48116_at	Cluster Incl. AI096389:qb91f12.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1707503 /clone_end=3' /gb=AI096389 /gi=3446300 /ug=Hs.110341 /len=566'	0.17789649	0.000023
51122_at	Cluster Incl. AI689756:tx30h05.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2271129 /clone_end=3' /gb=AI689756 /gi=4901050 /ug=Hs.26244 /len=542'	0.177272252	0.000009

Table 3. U95_B Fold Change Genes (>3 over-expressed in Barrett's associated esophageal adenocarcinoma (BA), <0.33 under-expressed in BA)

Affy ID	Gene Name	Fold Change	P-value
50729_at	Cluster Incl. N39954:yyw69f12.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-257519 /clone_end=5' /gb=N39954 /gi=1163499 /ug=Hs.109012 /len=531'	0.174253817	0.000343
53970_at	Cluster Incl. AF150266:AF150266 Homo sapiens cDNA /clone=CBFBIG05 /gb=AF150266 /gi=5133702 /ug=Hs.62643 /len=1425	0.17406147	0.000039
55697_at	Cluster Incl. AL653211:wb23h04.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2306551 /clone_end=3' /gb=AL653211 /gi=4737190 /ug=Hs.96657 /len=620'	0.173630297	0.009509
47597_at	Cluster Incl. AL040944:DKFZp434K2415_s1 Homo sapiens cDNA, 3 end /clone=DKFZp434K2415 /clone_end=3' /gb=AL040944 /gi=5409888 /ug=Hs.96937 /len=768'	0.173346375	0.01163
55772_at	Cluster Incl. AL765963:wh69g08.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2386046 /clone_end=3' /gb=AL765963 /gi=5232472 /ug=Hs.10299 /len=518'	0.171422781	0.000022
43961_s_at	Cluster Incl. AL627648:ty81b09.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2285465 /clone_end=3' /gb=AL627648 /gi=4664448 /ug=Hs.26168 /len=754'	0.171272429	0.000004
45757_at	Cluster Incl. W73855:zd52f10.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-344299 /clone_end=5' /gb=W73855 /gi=1384028 /ug=Hs.32343 /len=677'	0.16034244	0.000246
48070_at	Cluster Incl. AL743780:wg53g09.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2368864 /clone_end=3' /gb=AL743780 /gi=5112068 /ug=Hs.107203 /len=529'	0.155837517	0.000073
44392_at	Cluster Incl. H07855:yl86a02.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-44907 /clone_end=3' /gb=H07855 /gi=872677 /ug=Hs.30604 /len=430'	0.150341872	0.000005
50891_at	Cluster Incl. AL768853:wj12f11.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2402637 /clone_end=3' /gb=AL768853 /gi=5235362 /ug=Hs.134478 /len=451'	0.149604741	0.00915
48486_at	Cluster Incl. AW024960:wu70c08.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-991041 /clone_end=3' /gb=AW024960 /gi=5878490 /ug=Hs.110945 /len=806'	0.149120971	0.000082
52955_at	Cluster Incl. T68813:yc29f09.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-82121 /clone_end=5' /gb=T68813 /gi=679961 /ug=Hs.11896 /len=583'	0.148934239	0.000064
52637_g_a	Cluster Incl. AW025596:wu75d09.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-990756 /clone_end=3' /gb=AW025596 /gi=5879126 /ug=Hs.238927 /len=488'	0.14616299	0.00001
46108_at	Cluster Incl. AL804914:tu43d04.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2253799 /clone_end=3' /gb=AL804914 /gi=5391504 /ug=Hs.55565 /len=535'	0.145421966	0.000387

Table 3. U95_B Fold Change Genes (>3 over-expressed in Barrett's associated esophageal adenocarcinoma (BA), <0.33 under-expressed in BA)

Affy ID	Gene Name	Fold Change	P-value
54066_at	Cluster Incl. AI356291:qz25h11.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2027973 /clone_end=3' /gb=AI356291 /gi=4107912 /ug=Hs.6775 /len=753'	0.143940201	0.000279
44113_at	Cluster Incl. U55984:HSU55984 Homo sapiens cDNA /clone=37941 /gb=U55984 /gi=1354540 /ug=Hs.26662 /len=1147	0.143500649	0
52049_at	Cluster Incl. AI742029:wg38b07.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2367349 /clone_end=3' /gb=AI742029 /gi=5110317 /ug=Hs.4232 /len=769'	0.141341539	0.000017
48293_at	Cluster Incl. AI128031:qc42h07.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1712317 /clone_end=3' /gb=AI128031 /gi=3596545 /ug=Hs.87383 /len=503'	0.140884301	0.010169
45220_at	Cluster Incl. AA150501:zi08g02.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-491762 /clone_end=3' /gb=AA150501 /gi=1722015 /ug=Hs.43148 /len=645'	0.136941145	0.000008
44104_at	Cluster Incl. AL036582:DKFZp564L0462.s1 Homo sapiens cDNA, 3 end /clone=DKFZp564L0462 /clone_end=3' /gb=AL036582 /gi=5927810 /ug=Hs.25740 /len=582'	0.135894846	0.000009
51261_at	Cluster Incl. AI052020:oy29e06.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1667266 /clone_end=3' /gb=AI052020 /gi=3308011 /ug=Hs.3593 /len=757'	0.135142446	0.000016
52986_at	Cluster Incl. AI743925:wg54f04.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2368927 /clone_end=3' /gb=AI743925 /gi=5112213 /ug=Hs.4944 /len=505'	0.134644236	0.000003
47328_at	Cluster Incl. AA483389:ne74d10.s1 Homo sapiens cDNA /clone=IMAGE-910003 /gb=AA483389 /gi=2212202 /ug=Hs.58566 /len=486	0.134567862	0.000026
55924_at	Cluster Incl. AA085776:zk71h10.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-488323 /clone_end=3' /gb=AA085776 /gi=1629238 /ug=Hs.68784 /len=633'	0.130253189	0.000015
56474_at	Cluster Incl. W23068:78H5 Homo sapiens cDNA /clone=(not-directional) /gb=W23068 /gi=1299950 /ug=Hs.111676 /len=627	0.128217729	0.002301
50607_at	Cluster Incl. R41725:yg11b02.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-31813 /clone_end=3' /gb=R41725 /gi=817432 /ug=Hs.140852 /len=437'	0.123861065	0.000016
55249_at	Cluster Incl. W69365:zd46f09.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-343721 /clone_end=3' /gb=W69365 /gi=1378676 /ug=Hs.58006 /len=446'	0.122494713	0
45684_at	Cluster Incl. AL040936:DKFZp434K1715.s1 Homo sapiens cDNA, 3 end /clone=DKFZp434K1715 /clone_end=3' /gb=AL040936 /gi=5409880 /ug=Hs.5027 /len=742'	0.122114371	0.000002

Table 3. U95_B Fold Change Genes (>3 over-expressed in Barrett's associated esophageal adenocarcinoma (BA), <0.33 under-expressed in BA)

Affy ID	Gene Name	Fold Change	P-value
47385_at	Cluster Incl. A1147256:qb36h11.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1698405 /clone_end=3' /gb=A1147256 /gi=3674938 /ug=Hs.61460 /len=436'	0.121799678	0.000003
51096_at	Cluster Incl. AL048651:DKFZp564O2171_s1 Homo sapiens cDNA /clone=DKFZp564O2171 /gb=AL048651 /gi=4727712 /ug=Hs.25740 /len=840	0.118284422	0.000009
47032_at	Cluster Incl. AI885390:wI93c03.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2432452 /clone_end=3' /gb=AI885390 /gi=5590554 /ug=Hs.49031 /len=575'	0.11658742	0.000001
57685_at	Cluster Incl. AI669815:tu31f07.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2252677 /clone_end=3' /gb=AI669815 /gi=4834589 /ug=Hs.129911 /len=646'	0.114663319	0.002628
51289_at	Cluster Incl. C00414:HUMGS0005283 Homo sapiens cDNA /gb=C00414 /gi=1432644 /ug=Hs.37331 /len=546	0.114661173	0.001594
53593_at	Cluster Incl. AI494498:qz01a06.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2020210 /clone_end=3' /gb=AI494498 /gi=4395501 /ug=Hs.44685 /len=450'	0.112799017	0
55491_at	Cluster Incl. AI081571:ox59h10.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1660675 /clone_end=3' /gb=AI081571 /gi=3418363 /ug=Hs.96457 /len=468'	0.111799777	0.000002
51939_at	Cluster Incl. AA142913:zI40e07.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-504420 /clone_end=3' /gb=AA142913 /gi=1712300 /ug=Hs.71721 /len=572'	0.111488827	0.000898
51837_at	Cluster Incl. AI916261:wg99d02.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2379363 /clone_end=3' /gb=AI916261 /gi=5636116 /ug=Hs.55409 /len=842'	0.109272217	0
55278_at	Cluster Incl. AI659657:tu25b10.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2252059 /clone_end=3' /gb=AI659657 /gi=4763227 /ug=Hs.58561 /len=678'	0.103460982	0.000001
43431_at	Cluster Incl. AW006202:wz93e02.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2566394 /clone_end=3' /gb=AW006202 /gi=5854980 /ug=Hs.235162 /len=539'	0.10274855	0.004097
46104_at	Cluster Incl. AA772055:ai41e03.s1 Homo sapiens cDNA, 3 end /clone=1359580 /clone_end=3' /gb=AA772055 /gi=2823838 /ug=Hs.55314 /len=504'	0.098385581	0.000009
51071_at	Cluster Incl. N49836:yz08a11.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-282428 /clone_end=3' /gb=N49836 /gi=1191002 /ug=Hs.46969 /len=638'	0.096194999	0
47929_at	Cluster Incl. AI097310:qb35a09.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1698232 /clone_end=3' /gb=AI097310 /gi=3446892 /ug=Hs.165240 /len=476'	0.083211562	0.000054
44613_at	Cluster Incl. AI681917:tx50f03.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2273021 /clone_end=3' /gb=AI681917 /gi=4892099 /ug=Hs.3321 /len=711'	0.082599471	0.000147

Table 3. U95_B Fold Change Genes (>3 over-expressed in Barrett's associated esophageal adenocarcinoma (BA), <0.33 under-expressed in BA)

Affy ID	Gene Name	Fold Change	P-value
46924_at	Cluster Incl. AI824107: wj46c09.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2405872 /clone_end=3' /gb=AI824107 /gi=5444778 /ug=Hs.55408 /len=589'	0.081634712	0.000003
55436_at	Cluster Incl. AI669212: wc13c10.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2315058 /clone_end=3' /gb=AI669212 /gi=4833986 /ug=Hs.92127 /len=596'	0.069851384	0.000001
49925_at	Cluster Incl. AI971227: wr26g05.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2488856 /clone_end=3' /gb=AI971227 /gi=5768053 /ug=Hs.104266 /len=545'	0.066652473	0.000018
54445_at	Cluster Incl. AA531023: nj07e04.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-985662 /clone_end=3' /gb=AA531023 /gi=2273729 /ug=Hs.59771 /len=611'	0.065598325	0.000095
46172_at	Cluster Incl. AI142832: qa26f12.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1687919 /clone_end=3' /gb=AI142832 /gi=3659191 /ug=Hs.61232 /len=571'	0.064763267	0
54005_at	Cluster Incl. AI082067: oz52f09.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1678985 /clone_end=3' /gb=AI082067 /gi=3418859 /ug=Hs.64746 /len=629'	0.064237546	0.000001
50877_at	Cluster Incl. AA351682: EST59783 Homo sapiens cDNA, 3 end /clone=ATCC-152104 /clone_end=3' /gb=AA351682 /gi=2004217 /ug=Hs.12714 /len=415'	0.059597786	0.000008
56607_at	Cluster Incl. AA195677: zr32h04.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-665143 /clone_end=3' /gb=AA195677 /gi=1785355 /ug=Hs.86023 /len=475'	0.058208329	0.000001
47119_at	Cluster Incl. AA130221: zl37h09.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-504161 /clone_end=5' /gb=AA130221 /gi=1691225 /ug=Hs.87013 /len=595'	0.044591279	0.000022
47941_at	Cluster Incl. AI540870: PEC1.2_07_G11.r Homo sapiens cDNA, 5 end /clone_end=5' /gb=AI540870 /gi=4458243 /ug=Hs.16740 /len=862'	0.036240181	0.00003
51669_r_at	Cluster Incl. AA583578: nn61c02.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1088354 /clone_end=3' /gb=AA583578 /gi=2368187 /ug=Hs.185158 /len=306'	0.035202429	0.000027
53747_at	Cluster Incl. AA422178: zv31g07.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-755292 /clone_end=5' /gb=AA422178 /gi=2101029 /ug=Hs.124660 /len=503'	0.034458051	0.000093
51214_at	Cluster Incl. AI378979: tc40d07.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2067085 /clone_end=3' /gb=AI378979 /gi=4188832 /ug=Hs.32426 /len=527'	0.02696214	0.0002
47448_at	Cluster Incl. R37637: yf61b01.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-26665 /clone_end=3' /gb=R37637 /gi=795093 /ug=Hs.12286 /len=460'	0.022494655	0.00001

Table 3. U95_B Fold Change Genes (>3 over-expressed in Barrett's associated esophageal adenocarcinoma (BA), <0.33 under-expressed in BA)

Affy ID	Gene Name	Fold Change	P-value
46163_at	Cluster Incl. A1692575:wd73h12.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2337287 /clone_end=3' /gb=A1692575 /gi=4969915 /ug=Hs.59761 /len=493'	0.021738726	0.000026

Table 4. U95_C Fold Change Genes (>3 over-expressed in Barrett's associated esophageal adenocarcinoma (BA), <0.33 under-expressed in BA)

Affy ID	Gene Name	Fold Change	P-value
64472_at	Cluster Incl. AA877900:nt12g08.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1161662 /clone_end=3' /gb=AA877900 /gi=2986865 /ug=Hs.5940 /len=580'	20.2668142	0.000019
60504_at	Cluster Incl. AI859849:wm21c04.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2436582 /clone_end=3' /gb=AI859849 /gi=5513454 /ug=Hs.184598 /len=507'	16.18781039	0.000015
48774_at	Cluster Incl. AA584310:nt79g01.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1090128 /clone_end=3' /gb=AA584310 /gi=2368919 /ug=Hs.99769 /len=582'	13.20890926	0.000632
65626_at	Cluster Incl. AA059458:z196g05.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-512504 /clone_end=5' /gb=AA059458 /gi=1553317 /ug=Hs.28792 /len=572'	9.104795333	0.000345
48797_at	Cluster Incl. AI346914:qp59c05.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1927304 /clone_end=3' /gb=AI346914 /gi=4084120 /ug=Hs.105484 /len=725'	8.180270082	0.001096
61671_at	Cluster Incl. AA194980:zr35f09.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-665417 /clone_end=5' /gb=AA194980 /gi=1784901 /ug=Hs.30818 /len=585'	7.888195657	0.000433
61429_at	Cluster Incl. AI948490:wq06e01.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2470488 /clone_end=3' /gb=AI948490 /gi=5740800 /ug=Hs.98765 /len=617'	7.811425507	0.000148
57224_s	Cluster Incl. AI983033:wz30a12.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2559550 /clone_end=3' /gb=AI983033 /gi=5810252 /ug=Hs.233739 /len=456'	7.602018897	0.002796
61110_at	Cluster Incl. AA679297:zi28c04.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-432102 /clone_end=3' /gb=AA679297 /gi=2659819 /ug=Hs.234505 /len=564'	7.48284531	0.000022
63382_at	Cluster Incl. AI073984:oy66c05.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1670792 /clone_end=3' /gb=AI073984 /gi=3400628 /ug=Hs.14453 /len=585'	7.482353067	0.000367
65744_at	Cluster Incl. W58252:zd25d01.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-341665 /clone_end=5' /gb=W58252 /gi=1365194 /ug=Hs.182793 /len=614'	7.461285225	0.000186
60585_at	Cluster Incl. N63181:yz85d07.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-289837 /clone_end=3' /gb=N63181 /gi=1211010 /ug=Hs.48729 /len=479'	7.363840433	0.000614
51129_s	Cluster Incl. AI436136:ti15h07.y1 Homo sapiens cDNA, 5 end /clone=IMAGE-2130589 /clone_end=5' /gb=AI436136 /gi=4308073 /ug=Hs.237278 /len=525'	7.144984025	0.001259

Table 4. U95_C Fold Change Genes (>3 over-expressed in Barrett's associated esophageal adenocarcinoma (BA), <0.33 under-expressed in BA)

Affy ID	Gene Name	Fold Change	P-value
48777_at	Cluster Incl. N23796:yx36a10.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-263802 /clone_end=5' /gb=N23796 /gi=1137946 /ug=Hs.100132 /len=573'	7.055961732	0.001113
52429_at	Cluster Incl. AA583350:nn45h04.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1086871 /clone_end=3' /gb=AA583350 /gi=2367959 /ug=Hs.30701 /len=494'	7.004425205	0.001398
65264_at	Cluster Incl. A1306471:qn13b01.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1898089 /clone_end=3' /gb=A1306471 /gi=3989542 /ug=Hs.151334 /len=397'	6.697303594	0.000258
64408_s	Cluster Incl. AW025529:wu97d12.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-990954 /clone_end=3' /gb=AW025529 /gi=5879059 /ug=Hs.47536 /len=661'	6.635144195	0.000009
63335_at	Cluster Incl. A1285531:qu49b04.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1968079 /clone_end=3' /gb=A1285531 /gi=3923764 /ug=Hs.106260 /len=598'	6.550211507	0.000055
65963_at	Cluster Incl. W72043:zd66d01.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-345601 /clone_end=3' /gb=W72043 /gi=1382313 /ug=Hs.84628 /len=604'	6.462494702	0.000108
50926_s	Cluster Incl. R54585:yg81f12.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-39892 /clone_end=3' /gb=R54585 /gi=816487 /ug=Hs.233799 /len=493'	6.26291301	0.001886
49102_at	Cluster Incl. AA670193:af51d07.s1 Homo sapiens cDNA, 3 end /clone=1035181 /clone_end=3' /gb=AA670193 /gi=2631692 /ug=Hs.8687 /len=599'	6.242787256	0.002755
57830_s	Cluster Incl. AW024474:wu76h03.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-990888 /clone_end=3' /gb=AW024474 /gi=5878004 /ug=Hs.236884 /len=229'	6.116453605	0.009079
62959_at	Cluster Incl. AA204719:zq84c03.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-648292 /clone_end=3' /gb=AA204719 /gi=1802700 /ug=Hs.86327 /len=576'	5.981172544	0.000101
62952_at	Cluster Incl. AA480075:zv42b06.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-756275 /clone_end=5' /gb=AA480075 /gi=2208226 /ug=Hs.85015 /len=588'	5.866713492	0.000011
65792_at	Cluster Incl. AA526079:ni94d02.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-984483 /clone_end=3' /gb=AA526079 /gi=2268148 /ug=Hs.234180 /len=551'	5.682858552	0.002038
65128_at	Cluster Incl. A1915649:wg74a06.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2370802 /clone_end=3' /gb=A1915649 /gi=5635558 /ug=Hs.11638 /len=716'	5.678364543	0.000005
57223_at	Cluster Incl. A1982768:wu16a03.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2517100 /clone_end=3' /gb=A1982768 /gi=5809987 /ug=Hs.233732 /len=292'	5.672386526	0.000027

Table 4. U95_C Fold Change Genes (>3 over-expressed in Barrett's associated esophageal adenocarcinoma (BA), <0.33 under-expressed in BA)

Affy ID	Gene Name	Fold Change	P-value
55210_at	Cluster Incl. AI394117:tg21g11.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2109476 /clone_end=3' /gb=AI394117 /gi=4223664 /ug=Hs.156339 /len=251'	5.644425711	0.001741
56599_i_a	Cluster Incl. AI005676:ov59f10.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1641643 /clone_end=3' /gb=AI005676 /gi=3215186 /ug=Hs.237762 /len=491'	5.45726309	0.010029
57084_s	Cluster Incl. AW009817:ws87h04.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2504983 /clone_end=3' /gb=AW009817 /gi=5858595 /ug=Hs.236097 /len=440'	5.442500182	0.03874
65339_r_a	Cluster Incl. AA004528:zh91a09.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-428632 /clone_end=3' /gb=AA004528 /gi=1448105 /ug=Hs.169444 /len=415'	5.431448971	0.000043
64246_at	Cluster Incl. AI660247:we68h08.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2346303 /clone_end=3' /gb=AI660247 /gi=4763817 /ug=Hs.32699 /len=601'	5.427125242	0.000386
65155_at	Cluster Incl. AA707308:zj27a11.s1 Homo sapiens cDNA, 3 end /clone=451484 /clone_end=3' /gb=AA707308 /gi=2717226 /ug=Hs.12369 /len=566'	5.423294999	0.000008
63307_at	Cluster Incl. AL041566:DKFZp43410217_s1 Homo sapiens cDNA, 3 end /clone=DKFZp43410217 /clone_end=3' /gb=AL041566 /gi=5420916 /ug=Hs.100747 /len=715'	5.414527108	0.000272
51758_s	Cluster Incl. N21439:yx58f02.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-265947 /clone_end=3' /gb=N21439 /gi=1126609 /ug=Hs.238941 /len=510'	5.412633228	0.000095
48744_g	Cluster Incl. AA612678:nq25e10.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1144938 /clone_end=3' /gb=AA612678 /gi=2463716 /ug=Hs.95583 /len=565'	5.282186627	0.000486
64740_at	Cluster Incl. AA470369:ne10a12.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-880798 /clone_end=3' /gb=AA470369 /gi=2197678 /ug=Hs.72115 /len=708'	5.272312377	0.00136
65516_at	Cluster Incl. AA883422:am25a05.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1467824 /clone_end=3' /gb=AA883422 /gi=2992952 /ug=Hs.18791 /len=714'	5.212802857	0.005655
60071_s	Cluster Incl. AI961907:wt40f10.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2509963 /clone_end=3' /gb=AI961907 /gi=5754620 /ug=Hs.239230 /len=448'	5.197556431	0.000125
65883_at	Cluster Incl. AI954159:wx80e01.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2549976 /clone_end=3' /gb=AI954159 /gi=5746469 /ug=Hs.47622 /len=534'	5.022448143	0.003175
63927_f_a	Cluster Incl. AI963642:wr64b03.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2492429 /clone_end=3' /gb=AI963642 /gi=5756281 /ug=Hs.231969 /len=577'	4.776630548	0.000532

Table 4. U95_C Fold Change Genes (>3 over-expressed in Barrett's associated esophageal adenocarcinoma (BA), <0.33 under-expressed in BA)

Affy ID	Gene Name	Fold Change	P-value
63673_at	Cluster Incl. AI635057:tz03g09.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2287552 /clone_end=3' /gb=AI635057 /gi=4686387 /ug=Hs.200030 /len=703'	4.699661783	0.016394
62565_at	Cluster Incl. W21872:57h7 Homo sapiens cDNA /clone=(not-directional) /gb=W21872 /gi=1298705 /ug=Hs.7907 /len=773	4.639766922	0.001581
65015_at	Cluster Incl. AI092131:qa59g12.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1691110 /clone_end=3' /gb=AI092131 /gi=3431125 /ug=Hs.11210 /len=529'	4.631614099	0.00018
61881_at	Cluster Incl. AA675917:e03503f Homo sapiens cDNA, 3 end /clone=e03503 /clone_end=3' /gb=AA675917 /gi=2775264 /ug=Hs.120912 /len=787'	4.514486314	0.000292
65645_at	Cluster Incl. AI675886:wc06f12.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2314415 /clone_end=3' /gb=AI675886 /gi=4876366 /ug=Hs.30299 /len=590'	4.50874656	0.000061
65578_at	Cluster Incl. AI817147:wg62c06.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2369674 /clone_end=3' /gb=AI817147 /gi=5436226 /ug=Hs.238105 /len=763'	4.446160162	0.000109
59510_at	Cluster Incl. AI832076:td12b02.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2075403 /clone_end=3' /gb=AI832076 /gi=5452747 /ug=Hs.127305 /len=734'	4.330867004	0.001152
54839_at	Cluster Incl. N51702:yy72d03.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-279077 /clone_end=3' /gb=N51702 /gi=1192868 /ug=Hs.101392 /len=514'	4.278675286	0.040746
63596_f_a	Cluster Incl. AI983633:wf50b06.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2510867 /clone_end=3' /gb=AI983633 /gi=5810852 /ug=Hs.233757 /len=610'	4.226128442	0.000841
64504_r_a	Cluster Incl. AA868136:ak45g12.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1408966 /clone_end=3' /gb=AA868136 /gi=2963581 /ug=Hs.238884 /len=306'	4.175057561	0.001777
62240_at	Cluster Incl. AI096692:qb91b06.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1707443 /clone_end=3' /gb=AI096692 /gi=3446186 /ug=Hs.157461 /len=447'	4.173231366	0.000007
62467_at	Cluster Incl. W63576:zc55h09.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-326273 /clone_end=5' /gb=W63576 /gi=1371149 /ug=Hs.58093 /len=604'	4.112846813	0.000093
54444_at	Cluster Incl. AA862350:og94c06.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1455946 /clone_end=3' /gb=AA862350 /gi=2954829 /ug=Hs.96151 /len=590'	4.090071897	0.004216
64454_at	Cluster Incl. AI805943:te52h02.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2090355 /clone_end=3' /gb=AI805943 /gi=5392509 /ug=Hs.5723 /len=772'	4.013492489	0.021332

Table 4. U95_C Fold Change Genes (>3 over-expressed in Barrett's associated esophageal adenocarcinoma (BA), <0.33 under-expressed in BA)

Affy ID	Gene Name	Fold Change	P-value
64702_at	Cluster Incl. AI809005:wf67f06.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2360675 /clone_end=3' /gb=AI809005 /gi=5395571 /ug=Hs.50883 /len=596'	4.009878713	0.000142
61943_at	Cluster Incl. AI262104:qz28d10.y1 Homo sapiens cDNA, 5 end /clone=IMAGE-2028211 /clone_end=5' /gb=AI262104 /gi=3870307 /ug=Hs.140932 /len=523'	3.992422378	0.000194
62695_at	Cluster Incl. AA502331:ne26h06.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-898523 /clone_end=3' /gb=AA502331 /gi=2237298 /ug=Hs.15951 /len=534'	3.975578279	0.009789
64514_at	Cluster Incl. AI811865:tw45f01.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2262649 /clone_end=3' /gb=AI811865 /gi=5398431 /ug=Hs.239080 /len=401'	3.900924095	0.003286
60860_f a	Cluster Incl. AI086805:oz57e06.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1679458 /clone_end=3' /gb=AI086805 /gi=3425228 /ug=Hs.233789 /len=420'	3.889966281	0.003683
65690_at	Cluster Incl. AI091277:ow62b07.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1651381 /clone_end=3' /gb=AI091277 /gi=3430336 /ug=Hs.32659 /len=692'	3.881822704	0.002192
60082_s	Cluster Incl. AI991395:ws09f02.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2496699 /clone_end=3' /gb=AI991395 /gi=5838300 /ug=Hs.239944 /len=300'	3.80225973	0.008484
64735_at	Cluster Incl. AI684745:wa85f09.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2302985 /clone_end=3' /gb=AI684745 /gi=4896039 /ug=Hs.6952 /len=652'	3.799796162	0.031697
65139_at	Cluster Incl. AI925240:wn52d12.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2449079 /clone_end=3' /gb=AI925240 /gi=5661204 /ug=Hs.118983 /len=494'	3.79978649	0.000677
64742_at	Cluster Incl. AI638445:tt07a10.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2240058 /clone_end=3' /gb=AI638445 /gi=4690679 /ug=Hs.72484 /len=718'	3.799745386	0.038879
60797_at	Cluster Incl. AI076180:oz01f06.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1674083 /clone_end=3' /gb=AI076180 /gi=3405358 /ug=Hs.214410 /len=603'	3.77504304	0.005248
64258_f a	Cluster Incl. AW016235:UI-H-BI0p-abl-a-06-0-UI.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-2712083 /clone_end=3' /gb=AW016235 /gi=5864992 /ug=Hs.234283 /len=438'	3.774669144	0.002065
65572_at	Cluster Incl. AI635827:tz81d05.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2294985 /clone_end=3' /gb=AI635827 /gi=4687157 /ug=Hs.23723 /len=709'	3.740835788	0.016428
48664_at	Cluster Incl. AI762879:wf63d05.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2397993 /clone_end=3' /gb=AI762879 /gi=5178546 /ug=Hs.86437 /len=604'	3.728590312	0.00008

Table 4. U95_C Fold Change Genes (>3 over-expressed in Barrett's associated esophageal adenocarcinoma (BA), <0.33 under-expressed in BA)

Affy ID	Gene Name	Fold Change	P-value
61126_at	Cluster Incl. N22262: yw36c04.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-254310 /clone_end=3' /gb=N22262 /gi=1128396 /ug=Hs.30779 /len=447'	3.726525355	0.000113
63994_i_a	Cluster Incl. AW006898: ws15g04.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2497302 /clone_end=3' /gb=AW006898 /gi=5855676 /ug=Hs.234094 /len=228'	3.685571992	0.020562
62997_at	Cluster Incl. A1972895: wr44h09.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2490593 /clone_end=3' /gb=A1972895 /gi=5769721 /ug=Hs.91226 /len=594'	3.675466573	0.006908
51097_at	Cluster Incl. AW003232: wq64c12.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2476054 /clone_end=3' /gb=AW003232 /gi=5850148 /ug=Hs.236518 /len=683'	3.647036307	0.003288
58825_at	Cluster Incl. A1701911: tq19f05.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2209281 /clone_end=3' /gb=A1701911 /gi=4989811 /ug=Hs.236455 /len=431'	3.636855749	0.009978
50183_at	Cluster Incl. A1347165: tc04d10.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2062867 /clone_end=3' /gb=A1347165 /gi=4084371 /ug=Hs.71561 /len=535'	3.626154256	0.005991
65797_at	Cluster Incl. AA127736: zk88c12.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-489910 /clone_end=5' /gb=AA127736 /gi=1687099 /ug=Hs.237523 /len=616'	3.610269552	0.001966
53261_at	Cluster Incl. A1337231: qx83h10.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2009155 /clone_end=3' /gb=A1337231 /gi=4074158 /ug=Hs.50115 /len=484'	3.583182611	0.000578
62536_at	Cluster Incl. AA527180: ni20b09.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-968537 /clone_end=3' /gb=AA527180 /gi=2269249 /ug=Hs.67928 /len=577'	3.56570974	0.001133
56784_at	Cluster Incl. A1016894: ou31c06.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1627882 /clone_end=3' /gb=A1016894 /gi=3231230 /ug=Hs.45204 /len=431'	3.557237251	0.001861
57027_at	Cluster Incl. A1990405: ws20h10.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2497795 /clone_end=3' /gb=A1990405 /gi=5837286 /ug=Hs.233881 /len=481'	3.547382938	0.00167
61638_at	Cluster Incl. AA700160: zj36h03.s1 Homo sapiens cDNA, 3 end /clone=452405 /clone_end=3' /gb=AA700160 /gi=2703123 /ug=Hs.28564 /len=502'	3.543445756	0.000324
60950_f_a	Cluster Incl. AA741117: nz04f09.s1 Homo sapiens cDNA /clone=IMAGE-1286825 /gb=AA741117 /gi=2779709 /ug=Hs.78684 /len=466	3.543004523	0.000039
62950_at	Cluster Incl. W84421: zd89g04.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-356694 /clone_end=3' /gb=W84421 /gi=1395562 /ug=Hs.83992 /len=648'	3.487421091	0.000644

Table 4. U95_C Fold Change Genes (>3 over-expressed in Barrett's associated esophageal adenocarcinoma (BA), <0.33 under-expressed in BA)

Affy ID	Gene Name	Fold Change	P-value
58848_at	Cluster Incl. A1809489:wf30b04.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2357071 /clone_end=3' /gb=A1809489 /gi=5396055 /ug=Hs.236580 /len=787	3.471887883	0.007471
64274_at	Cluster Incl. A1766469:wf41a06.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2392786 /clone_end=3' /gb=A1766469 /gi=5232978 /ug=Hs.234483 /len=337	3.471012959	0.020051
55678_at	Cluster Incl. W72885:zd59d05.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-344937 /clone_end=3' /gb=W72885 /gi=1383020 /ug=Hs.237652 /len=424	3.422525993	0.00455
62743_at	Cluster Incl. AA811088:oa85c12.s1 Homo sapiens cDNA /clone=IMAGE-1319062 /gb=AA811088 /gi=2880699 /ug=Hs.172581 /len=571	3.399387119	0.011542
65492_at	Cluster Incl. N56950:yy82g06.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-280090 /clone_end=3' /gb=N56950 /gi=1200840 /ug=Hs.172241 /len=602	3.365968673	0.00226
64144_at	Cluster Incl. AW026010:ww05e09.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-990875 /clone_end=3' /gb=AW026010 /gi=5879540 /ug=Hs.239812 /len=580	3.358826512	0.000172
58636_f_a	Cluster Incl. R33841:yh82a10.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-136218 /clone_end=3' /gb=R33841 /gi=789699 /ug=Hs.175011 /len=400	3.356616113	0.00199
49146_at	Cluster Incl. AA305101:EST176103 Homo sapiens cDNA, 5 end /clone=ATCC-128591 /clone_end=5' /gb=AA305101 /gi=1957429 /ug=Hs.107614 /len=547	3.33565472	0.020805
60006_at	Cluster Incl. A1816780:wj34a09.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2404696 /clone_end=3' /gb=A1816780 /gi=5435859 /ug=Hs.15088 /len=499	3.315740997	0.019201
48773_at	Cluster Incl. AA642981:gi=2568199 /ug=Hs.9960 /len=563	3.313599312	0.004231
53789_at	Cluster Incl. A1866583:tz51d04.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1172421 /clone_end=3' /gb=A1866583 /gi=5530690 /ug=Hs.74921 /len=479	3.313016769	0.001358
66186_at	Cluster Incl. Z41019:HSC2MC092 Homo sapiens cDNA, 3 end /clone=c-2mc09 /clone_end=3' /gb=Z41019 /gi=566764 /ug=Hs.113530 /len=317	3.303305427	0.000884
63800_at	Cluster Incl. AA195158:zr35f06.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-665411 /clone_end=5' /gb=AA195158 /gi=1784847 /ug=Hs.204154 /len=723	3.293703299	0.000004
50202_s	Cluster Incl. AA917667:on46d02.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1559715 /clone_end=3' /gb=AA917667 /gi=3057557 /ug=Hs.77365 /len=562	3.28918373	0.001767

Table 4. U95_C Fold Change Genes (>3 over-expressed in Barrett's associated esophageal adenocarcinoma (BA), <0.33 under-expressed in BA)

Affy ID	Gene Name	Fold Change	P-value
66585_at	Cluster Incl. AA879466:oj91h03.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1505717 /clone_end=3' /gb=AA879466 /gi=2988577 /ug=Hs.125427 /len=416'	3.285845033	0.019475
61448_at	Cluster Incl. AA766126:oa27f10.s1 Homo sapiens cDNA /clone=IMAGE-1306219 /gb=AA766126 /gi=2817364 /ug=Hs.99338 /len=398	3.275425186	0.000966
63124_at	Cluster Incl. AA631399:np86e09.s1 Homo sapiens cDNA /clone=IMAGE-1133224 /gb=AA631399 /gi=2554010 /ug=Hs.191512 /len=457	3.274156292	0.001603
57034_at	Cluster Incl. AW003626:wx34e02.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2545562 /clone_end=3' /gb=AW003626 /gi=5850542 /ug=Hs.234018 /len=707'	3.255247904	0.020433
49633_at	Cluster Incl. N21131:yx52g04.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-265398 /clone_end=3' /gb=N21131 /gi=1126301 /ug=Hs.233612 /len=571'	3.253214384	0.014949
60314_at	Cluster Incl. AI014820:of87f01.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1623769 /clone_end=3' /gb=AI014820 /gi=3229156 /ug=Hs.131756 /len=311'	3.249891116	0.001175
48746_at	Cluster Incl. AA527237:ng35e09.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-936808 /clone_end=3' /gb=AA527237 /gi=2269306 /ug=Hs.95583 /len=496'	3.24979003	0.016432
61941_at	Cluster Incl. AI701037:we09h11.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2340645 /clone_end=3' /gb=AI701037 /gi=4988937 /ug=Hs.139784 /len=586'	3.247978145	0.004021
61664_r a	Cluster Incl. AI859398:wm11a08.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2435606 /clone_end=3' /gb=AI859398 /gi=5513014 /ug=Hs.3046 /len=518'	3.236515692	0.008108
65443_at	Cluster Incl. AA085711:z183c09.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-511216 /clone_end=3' /gb=AA085711 /gi=1629467 /ug=Hs.15125 /len=630'	3.236087458	0.018668
59134_at	Cluster Incl. AA947258:od86c08.s1 Homo sapiens cDNA /clone=IMAGE-1374830 /gb=AA947258 /gi=3108511 /ug=Hs.127703 /len=277	3.223980919	0.002204
62214_at	Cluster Incl. AI583960:ts08g12.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2228038 /clone_end=3' /gb=AI583960 /gi=4569857 /ug=Hs.55918 /len=1056'	3.15598437	0.021671
48666_at	Cluster Incl. AA902949:ok43h08.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1516767 /clone_end=3' /gb=AA902949 /gi=3038072 /ug=Hs.86489 /len=546'	3.152741137	0.002793
64388_at	Cluster Incl. AI685200:wc70b09.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2323961 /clone_end=3' /gb=AI685200 /gi=4896494 /ug=Hs.44155 /len=652'	3.120427707	0.001253

Table 4. U95_C Fold Change Genes (>3 over-expressed in Barrett's associated esophageal adenocarcinoma (BA), <0.33 under-expressed in BA)

Affy ID	Gene Name	Fold Change	P-value
62602_at	Cluster Incl. AA418402:zv92f02.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-767259 /clone_end=3' /gb=AA418402 /gi=2080211 /ug=Hs.175034 /len=543'	3.097490531	0.007758
64668_at	Cluster Incl. AI983929:wz55g05.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2562008 /clone_end=3' /gb=AI983929 /gi=5811148 /ug=Hs.44087 /len=498'	3.095095738	0.001828
60521_at	Cluster Incl. AL043931:DKFZp434F1328.s1 Homo sapiens cDNA, 3 end /clone=DKFZp434F1328 /clone_end=3' /gb=AL043931 /gi=5432159 /ug=Hs.194208 /len=656'	3.089245265	0.005927
64078_at	Cluster Incl. AA156269:zo50c04.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-590310 /clone_end=3' /gb=AA156269 /gi=1727904 /ug=Hs.29383 /len=640'	3.083000622	0.001219
54843_at	Cluster Incl. AI807036:wf37d02.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2357763 /clone_end=3' /gb=AI807036 /gi=5393602 /ug=Hs.101619 /len=593'	3.064820883	0.000199
57704_at	Cluster Incl. H04885:y74a03.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-43628 /clone_end=5' /gb=H04885 /gi=868437 /ug=Hs.72363 /len=517'	3.049533011	0.020401
48799_at	Cluster Incl. AI569988:tr90f10.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2226379 /clone_end=3' /gb=AI569988 /gi=4533362 /ug=Hs.105547 /len=744'	3.034133542	0.004434
57697_at	Cluster Incl. AI445628:tfj08c06.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2140906 /clone_end=3' /gb=AI445628 /gi=4289541 /ug=Hs.70980 /len=486'	3.03160246	0.005747
49728_s	Cluster Incl. AI056993:oz06b07.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1674517 /clone_end=3' /gb=AI056993 /gi=3330782 /ug=Hs.239310 /len=536'	3.030939775	0.038552
64103_at	Cluster Incl. N22751:yx65d07.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-266605 /clone_end=3' /gb=N22751 /gi=1136901 /ug=Hs.34665 /len=632'	3.029370854	0.000031
64347_s	Cluster Incl. AW007256:wf54b12.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2511263 /clone_end=3' /gb=AW007256 /gi=5856034 /ug=Hs.237397 /len=631'	3.014120526	0.014055
54364_at	Cluster Incl. AI472136:tfj86a07.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2148372 /clone_end=3' /gb=AI472136 /gi=4334226 /ug=Hs.88801 /len=549'	3.013549569	0.010051
61626_at	Cluster Incl. AA534969:nf72h05.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-925497 /clone_end=3' /gb=AA534969 /gi=2279222 /ug=Hs.27536 /len=552'	0.329753477	0.005999
66390_at	Cluster Incl. AI302387:qn50g05.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1901720 /clone_end=3' /gb=AI302387 /gi=3961733 /ug=Hs.120568 /len=396'	0.329198527	0.000067

Table 4. U95_C Fold Change Genes (>3 over-expressed in Barrett's associated esophageal adenocarcinoma (BA), <0.33 under-expressed in BA)

Affy ID	Gene Name	Fold Change	P-value
66860_at	Cluster Incl. AA994029:ou42e09.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1628968 /clone_end=3' /gb=AA994029 /gi=3180574 /ug=Hs.129464 /len=471'	0.328178816	0.002065
64285_at	Cluster Incl. AI050855:oy47a05.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1668944 /clone_end=3' /gb=AI050855 /gi=3307660 /ug=Hs.234984 /len=427'	0.327569476	0.000116
48866_at	Cluster Incl. AA176945:zp36c10.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-611538 /clone_end=3' /gb=AA176945 /gi=1758103 /ug=Hs.111136 /len=710'	0.327322228	0.044146
54748_at	Cluster Incl. AI309007:qp0b04.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1915759 /clone_end=3' /gb=AI309007 /gi=4003878 /ug=Hs.152569 /len=424'	0.326909965	0.012793
65964_at	Cluster Incl. AA203147:zx57d05.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-446601 /clone_end=5' /gb=AA203147 /gi=1799005 /ug=Hs.8518 /len=889'	0.323997933	0.016279
62824_at	Cluster Incl. AI095360:oy17f06.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1666115 /clone_end=3' /gb=AI095360 /gi=3434336 /ug=Hs.148696 /len=428'	0.32360218	0.009552
60491_at	Cluster Incl. AA767440:nz82c02.s1 Homo sapiens cDNA /clone=IMAGE-1301954 /gb=AA767440 /gi=2818455 /ug=Hs.182882 /len=503	0.323586785	0.037968
57255_f_a	Cluster Incl. AI991501:ws17d09.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2497457 /clone_end=3' /gb=AI991501 /gi=5838406 /ug=Hs.233904 /len=290'	0.323023022	0.016114
62246_at	Cluster Incl. T92947:ye27b10.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-118939 /clone_end=3' /gb=T92947 /gi=724860 /ug=Hs.160999 /len=458'	0.322335146	0.001962
63972_at	Cluster Incl. AI985619:wr75e11.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2493548 /clone_end=3' /gb=AI985619 /gi=5812896 /ug=Hs.233813 /len=645'	0.321481527	0.012815
65471_at	Cluster Incl. AI744118:wc36e07.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2317284 /clone_end=3' /gb=AI744118 /gi=5112406 /ug=Hs.169575 /len=588'	0.319850405	0.03235
64684_at	Cluster Incl. AA528168:nh91g06.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-965914 /clone_end=3' /gb=AA528168 /gi=2270237 /ug=Hs.48401 /len=610'	0.318842345	0.006451
49175_at	Cluster Incl. AI887986:wm27b05.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2437137 /clone_end=3' /gb=AI887986 /gi=5593150 /ug=Hs.110978 /len=749'	0.317648541	0.004512
55882_at	Cluster Incl. AI492376:ti27c10.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2131698 /clone_end=3' /gb=AI492376 /gi=4393379 /ug=Hs.17572 /len=538'	0.316649054	0.009055

Table 4. U95_C Fold Change Genes (>3 over-expressed in Barrett's associated esophageal adenocarcinoma (BA), <0.33 under-expressed in BA)

Affy ID	Gene Name	Fold Change	P-value
64395_at	Cluster Incl. H10808:ym04c09.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-46861 /clone_end=5' /gb=H10808 /gi=875628 /ug=Hs.44978 /len=601'	0.316637145	0.004543
62555_at	Cluster Incl. A1623176:ts78b04.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2237359 /clone_end=3' /gb=A1623176 /gi=4648101 /ug=Hs.7392 /len=664'	0.316473366	0.040377
64526_at	Cluster Incl. AW051272:wy83e11.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2555180 /clone_end=3' /gb=AW051272 /gi=5913542 /ug=Hs.25214 /len=371'	0.315849581	0.038785
65796_at	Cluster Incl. A1859366:wm10f01.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2435545 /clone_end=3' /gb=A1859366 /gi=5512982 /ug=Hs.237336 /len=707'	0.315525138	0.007601
61700_at	Cluster Incl. A1922821:wo14d06.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2455307 /clone_end=3' /gb=A1922821 /gi=5658785 /ug=Hs.32433 /len=537'	0.315495682	0.004301
61870_g	Cluster Incl. A1494617:qz17a11.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2021756 /clone_end=3' /gb=A1494617 /gi=4395620 /ug=Hs.118211 /len=646'	0.315484967	0.007413
60510_at	Cluster Incl. AA772381:ai44c03.s1 Homo sapiens cDNA, 3 end /clone=1359844 /clone_end=3' /gb=AA772381 /gi=2824164 /ug=Hs.188429 /len=570'	0.314791598	0.011959
57738_at	Cluster Incl. AA195964:zp97c05.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-628136 /clone_end=5' /gb=AA195964 /gi=1791589 /ug=Hs.87278 /len=615'	0.314196784	0.007585
62793_at	Cluster Incl. A1821806:nr33c08.x5 Homo sapiens cDNA, 3 end /clone=IMAGE-1169774 /clone_end=3' /gb=A1821806 /gi=5440885 /ug=Hs.191846 /len=679'	0.313701611	0.000016
62707_at	Cluster Incl. N21031:yx46f05.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-264801 /clone_end=3' /gb=N21031 /gi=1126201 /ug=Hs.164779 /len=554'	0.311461874	0.0078
63026_at	Cluster Incl. AA886976:oi14h01.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1476529 /clone_end=3' /gb=AA886976 /gi=3002084 /ug=Hs.95821 /len=749'	0.310368296	0.00234
57240_f a	Cluster Incl. A1701742:we07g11.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2340452 /clone_end=3' /gb=A1701742 /gi=4989642 /ug=Hs.233791 /len=344'	0.308442897	0.002019
65185_g	Cluster Incl. AA015613:ze20f12.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-359567 /clone_end=3' /gb=AA015613 /gi=1476661 /ug=Hs.13766 /len=647'	0.306125434	0.000036
65591_at	Cluster Incl. N64681:yz87g05.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-290072 /clone_end=3' /gb=N64681 /gi=1212510 /ug=Hs.239120 /len=606'	0.303421174	0.022703

Table 4. U95_C Fold Change Genes (>3 over-expressed in Barrett's associated esophageal adenocarcinoma (BA), <0.33 under-expressed in BA)

Affy ID	Gene Name	Fold Change	P-value
65543_at	Cluster Incl. A1621225:ts77a11.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2237276 /clone_end=3' /gb=A1621225 /gi=4630351 /ug=Hs.22452 /len=582'	0.302382221	0.003525
63952_at	Cluster Incl. A1970855:wr20f09.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2488265 /clone_end=3' /gb=A1970855 /gi=5767681 /ug=Hs.233633 /len=590'	0.302306661	0.000153
65514_at	Cluster Incl. AA166678:zq41e08.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-632294 /clone_end=3' /gb=AA166678 /gi=1745133 /ug=Hs.18760 /len=673'	0.302069999	0.000394
62287_at	Cluster Incl. AW005044:wz94a11.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2566460 /clone_end=3' /gb=AW005044 /gi=5853822 /ug=Hs.167433 /len=731'	0.301869349	0.000105
65483_at	Cluster Incl. A1658928:tu07d08.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2250351 /clone_end=3' /gb=A1658928 /gi=4762498 /ug=Hs.17110 /len=530'	0.300258246	0.003195
64293_at	Cluster Incl. A1971000:wr22f07.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2488453 /clone_end=3' /gb=A1971000 /gi=5767826 /ug=Hs.235392 /len=524'	0.296907004	0.00001
56545_r_a	Cluster Incl. H77843:ys09f06.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-214307 /clone_end=3' /gb=H77843 /gi=1055932 /ug=Hs.117886 /len=331'	0.296894418	0.000655
54887_at	Cluster Incl. AA772278:ai42d03.s1 Homo sapiens cDNA, 3 end /clone=1359653 /clone_end=3' /gb=AA772278 /gi=2824061 /ug=Hs.104623 /len=529'	0.295982417	0.003958
56590_s	Cluster Incl. A1431800:ti25d06.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2131499 /clone_end=3' /gb=A1431800 /gi=4305717 /ug=Hs.237258 /len=517'	0.295067963	0.000049
60847_at	Cluster Incl. AA406400:zv12b07.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-753397 /clone_end=5' /gb=AA406400 /gi=2064401 /ug=Hs.22851 /len=509'	0.294009282	0.006324
62066_at	Cluster Incl. A1919146:ti34d10.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2242675 /clone_end=3' /gb=A1919146 /gi=5639093 /ug=Hs.147293 /len=174'	0.292800813	0.001503
54215_at	Cluster Incl. AA742993:ny20a12.s1 Homo sapiens cDNA /clone=IMAGE-1272286 /gb=AA742993 /gi=2782499 /ug=Hs.190470 /len=285	0.292648011	0.000982
65934_at	Cluster Incl. A1546910:PN2.1_10_A10.r Homo sapiens cDNA, 5 end /clone_end=5' /gb=A1546910 /gi=4464398 /ug=Hs.7499 /len=791'	0.292566334	0.000017
49394_at	Cluster Incl. AA909687:om47d05.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1544169 /clone_end=3' /gb=AA909687 /gi=3049092 /ug=Hs.132222 /len=530'	0.291700552	0.00198

Table 4. U95_C Fold Change Genes (>3 over-expressed in Barrett's associated esophageal adenocarcinoma (BA), <0.33 under-expressed in BA)

Affy ID	Gene Name	Fold Change	P-value
51763_at	Cluster Incl. AA621061:ag03g05.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1056248 /clone_end=3' /gb=AA621061 /gi=2525000 /ug=Hs.238944 /len=473'	0.29151259	0.001387
63998_at	Cluster Incl. AA587236:nn82c12.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1090390 /clone_end=3' /gb=AA587236 /gi=2398050 /ug=Hs.234146 /len=630'	0.291223086	0.000005
62502_at	Cluster Incl. C75510:C75510 Homo sapiens cDNA /clone=hbc7804 /gb=C75510 /gi=2366572 /ug=Hs.61933 /len=543	0.28932962	0.000001
64485_at	Cluster Incl. AA057445:zf57h11.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-381093 /clone_end=3' /gb=AA057445 /gi=1550086 /ug=Hs.6176 /len=576'	0.288246999	0.001207
65460_at	Cluster Incl. AI669827:tu31g09.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2252704 /clone_end=3' /gb=AI669827 /gi=4834601 /ug=Hs.16577 /len=593'	0.28784121	0.001679
63782_at	Cluster Incl. AW051353:wy89g06.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2555770 /clone_end=3' /gb=AW051353 /gi=5913623 /ug=Hs.184668 /len=577'	0.287832225	0.000028
56234_r_a	Cluster Incl. AA053401:z171b05.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-510033 /clone_end=3' /gb=AA053401 /gi=1544038 /ug=Hs.177526 /len=434'	0.287820353	0.00614
61241_at	Cluster Incl. AI636422:tz79c01.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2294784 /clone_end=3' /gb=AI636422 /gi=4687752 /ug=Hs.140491 /len=599'	0.287143194	0.006593
49579_at	Cluster Incl. H45299:yn99g07.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-176604 /clone_end=3' /gb=H45299 /gi=921351 /ug=Hs.19845 /len=476'	0.2861687	0.000328
65858_at	Cluster Incl. N49855:yz08h09.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-282497 /clone_end=3' /gb=N49855 /gi=1191021 /ug=Hs.33054 /len=633'	0.284532394	0.000034
66525_at	Cluster Incl. AI860791:wl05h02.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2424051 /clone_end=3' /gb=AI860791 /gi=5514407 /ug=Hs.124359 /len=379'	0.283827138	0.00039
59962_at	Cluster Incl. AI703476:we24f08.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2342055 /clone_end=3' /gb=AI703476 /gi=4991376 /ug=Hs.13214 /len=512'	0.283690542	0.000172
62716_at	Cluster Incl. H98970:yx11c05.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-261416 /clone_end=3' /gb=H98970 /gi=1123638 /ug=Hs.166659 /len=623'	0.282761935	0.020256
62115_at	Cluster Incl. H95265:yu20e07.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-234372 /clone_end=3' /gb=H95265 /gi=1102898 /ug=Hs.42053 /len=592'	0.282482023	0.017318

Table 4. U95_C Fold Change Genes (>3 over-expressed in Barrett's associated esophageal adenocarcinoma (BA), <0.33 under-expressed in BA)

Affy ID	Gene Name	Fold Change	P-value
49249_s	Cluster Incl. AA533079:nj19e12.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-992974 /clone_end=3' /gb=AA533079 /gi=2277175 /ug=Hs.136005 /len=549'	0.279331424	0.012289
49749_at	Cluster Incl. AA312110:EST182804 Homo sapiens cDNA, 5 end /clone=ATCC-159298 /clone_end=5' /gb=AA312110 /gi=1964438 /ug=Hs.239945 /len=455'	0.277737004	0.010242
48861_at	Cluster Incl. AA224174:zr15d10.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-663475 /clone_end=5' /gb=AA224174 /gi=1844838 /ug=Hs.111099 /len=452'	0.275987009	0.007743
63674_r_a	Cluster Incl. AI653782:ty01d02.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2277795 /clone_end=3' /gb=AI653782 /gi=4737761 /ug=Hs.201337 /len=548'	0.274034829	0.012693
60426_at	Cluster Incl. AL047117:DKFZp586C2218_r1 Homo sapiens cDNA, 5 end /clone=DKFZp586C2218 /clone_end=5' /gb=AL047117 /gi=5435160 /ug=Hs.169425 /len=646'	0.271993302	0.003974
64327_at	Cluster Incl. AW014889:U1-H-B10-aaf-b-11-0-U1.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-2709069 /clone_end=3' /gb=AW014889 /gi=5863646 /ug=Hs.236762 /len=565'	0.271558043	0.000001
53582_at	Cluster Incl. AI141151:qe19e12.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1739470 /clone_end=3' /gb=AI141151 /gi=3648608 /ug=Hs.58330 /len=426'	0.271415126	0.000269
56147_f_a	Cluster Incl. T86696:yd86e02.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-115130 /clone_end=3' /gb=T86696 /gi=715048 /ug=Hs.169968 /len=329'	0.270730916	0.004461
65577_at	Cluster Incl. AI870013:wl63g12.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2429638 /clone_end=3' /gb=AI870013 /gi=5543981 /ug=Hs.238049 /len=536'	0.270716848	0.016125
64451_at	Cluster Incl. AL048814:DKFZp434F1618_s1 Homo sapiens cDNA /clone=DKFZp434F1618 /gb=AL048814 /gi=4728123 /ug=Hs.5624 /len=634'	0.270363039	0.010424
59694_at	Cluster Incl. AI971396:wr04d08.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2480559 /clone_end=3' /gb=AI971396 /gi=5768222 /ug=Hs.234838 /len=624'	0.26973595	0.00008
65734_at	Cluster Incl. AI744109:wc36d09.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2317265 /clone_end=3' /gb=AI744109 /gi=5112397 /ug=Hs.180141 /len=828'	0.268508824	0.025575
63892_at	Cluster Incl. AI056075:ox46e08.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1659398 /clone_end=3' /gb=AI056075 /gi=3329941 /ug=Hs.239678 /len=490'	0.267200526	0.016718
AFFX-HU	M33197 Human glyceraldehyde-3-phosphate dehydrogenase (GAPDH) mRNA, complete cds (5', M, 3' represent transcript regions 5 prime, Middle, and 3 prime respectively)	0.266542141	0.018105

Table 4. U95_C Fold Change Genes (>3 over-expressed in Barrett's associated esophageal adenocarcinoma (BA), <0.33 under-expressed in BA)

Affy ID	Gene Name	Fold Change	P-value
54068_at	AA973035:op25g06.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1577914 /clone_end=3' /gb=AA973035 /gi=3148215 /ug=Hs.128271 /len=494'	0.265826141	0.002294
64094_at	Cluster Incl. A1123601:qa50d10.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1690195 /clone_end=3' /gb=A1123601 /gi=3539367 /ug=Hs.32580 /len=603'	0.26328184	0.003637
50936_g	Cluster Incl. AA454184:zx48a10.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-795450 /clone_end=3' /gb=AA454184 /gi=2167853 /ug=Hs.233805 /len=559'	0.257098922	0.000135
62972_at	Cluster Incl. W56118:zc56h04.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-326359 /clone_end=5' /gb=W56118 /gi=1358007 /ug=Hs.87747 /len=582'	0.257076447	0.016006
62297_at	Cluster Incl. AL048338:DKFZp586C1424_s1 Homo sapiens cDNA /clone=DKFZp586C1424 /gb=AL048338 /gi=4727478 /ug=Hs.167956 /len=805	0.253314399	0.002475
48751_at	Cluster Incl. W61000:zc99g11.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-339332 /clone_end=3' /gb=W61000 /gi=1367759 /ug=Hs.9578 /len=607'	0.252779772	0.007829
64095_at	Cluster Incl. AL046950:DKFZp586J1617_s1 Homo sapiens cDNA, 3 end /clone=DKFZp586J1617 /clone_end=3' /gb=AL046950 /gi=5435008 /ug=Hs.32675 /len=726'	0.252581936	0.026995
64544_at	Cluster Incl. AA157506:zo55d01.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-590785 /clone_end=3' /gb=AA157506 /gi=1729131 /ug=Hs.29003 /len=427'	0.252105997	0.000747
62942_at	Cluster Incl. A1346341:qp50b09.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1926425 /clone_end=3' /gb=A1346341 /gi=4083547 /ug=Hs.82669 /len=549'	0.251328324	0.000433
61639_at	Cluster Incl. AA863003:og99d06.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1456427 /clone_end=3' /gb=AA863003 /gi=2955482 /ug=Hs.28651 /len=455'	0.250029119	0.004024
63845_at	Cluster Incl. A1766309:wh71d09.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2386193 /clone_end=3' /gb=A1766309 /gi=5232818 /ug=Hs.23363 /len=571'	0.249268909	0.001144
66785_i_a	Cluster Incl. A1223376:qg43d08.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1837935 /clone_end=3' /gb=A1223376 /gi=3805579 /ug=Hs.128454 /len=387'	0.249160717	0.002653
52038_r_a	Cluster Incl. A1223016:qg52f04.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1838815 /clone_end=3' /gb=A1223016 /gi=3805219 /ug=Hs.144742 /len=281'	0.24791803	0.00541
56809_at	Cluster Incl. A1052524:oz27f07.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1676581 /clone_end=3' /gb=A1052524 /gi=3308515 /ug=Hs.4799 /len=537'	0.245992054	0.000385

Table 4. U95_C Fold Change Genes (>3 over-expressed in Barrett's associated esophageal adenocarcinoma (BA), <0.33 under-expressed in BA)

Affy ID	Gene Name	Fold Change	P-value
65175_at	Cluster Incl. A1741026:wg25e11.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2366156 /clone_end=3' /gb=A1741026 /gi=5109314 /ug=Hs.13299 /len=592'	0.2449656	0.000409
65893_at	Cluster Incl. A1151271:qc88b06.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1721267 /clone_end=3' /gb=A1151271 /gi=3679740 /ug=Hs.5243 /len=616'	0.24384702	0.001358
62692_at	Cluster Incl. AA410788:zi35b11.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-724317 /clone_end=5' /gb=AA410788 /gi=2069895 /ug=Hs.183673 /len=484'	0.243344597	0.006983
54730_at	Cluster Incl. AA553527:nk78a04.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1019598 /clone_end=3' /gb=AA553527 /gi=2324066 /ug=Hs.152432 /len=510'	0.242978961	0.000938
60481_i_a	Cluster Incl. AA932331:oo60a08.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1570550 /clone_end=3' /gb=AA932331 /gi=3086569 /ug=Hs.181174 /len=508'	0.241809966	0.006633
54556_at	Cluster Incl. A1554741:tn27g07.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2168892 /clone_end=3' /gb=A1554741 /gi=4487104 /ug=Hs.150657 /len=466'	0.241602147	0.003086
61247_f_a	Cluster Incl. R67332:yj32e02.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-140954 /clone_end=3' /gb=R67332 /gi=839970 /ug=Hs.140987 /len=423'	0.241131758	0.012114
60029_i_a	Cluster Incl. A1589514:tm57a12.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2162206 /clone_end=3' /gb=A1589514 /gi=4598562 /ug=Hs.15688 /len=493'	0.23979923	0.005698
56675_at	Cluster Incl. H28004:yj59g07.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-162588 /clone_end=3' /gb=H28004 /gi=898357 /ug=Hs.25699 /len=462'	0.235365417	0.000016
65113_at	Cluster Incl. A1952965:wq49d11.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2474613 /clone_end=3' /gb=A1952965 /gi=5745275 /ug=Hs.97837 /len=472'	0.234876957	0.001006
58434_at	Cluster Incl. A1268312:qm04b12.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1880831 /clone_end=3' /gb=A1268312 /gi=3887479 /ug=Hs.103009 /len=609'	0.233510248	0.000001
63311_at	Cluster Incl. A1742378:wg40c02.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2367554 /clone_end=3' /gb=A1742378 /gi=5110666 /ug=Hs.101514 /len=672'	0.232118688	0.004954
62573_at	Cluster Incl. H04627:yj49f04.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-152095 /clone_end=5' /gb=H04627 /gi=867560 /ug=Hs.79793 /len=576'	0.230460891	0.002567
62351_at	Cluster Incl. A1217310:qh25d09.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1845713 /clone_end=3' /gb=A1217310 /gi=3797125 /ug=Hs.147568 /len=390'	0.230064353	0.000264

Table 4. U95_C Fold Change Genes (>3 over-expressed in Barrett's associated esophageal adenocarcinoma (BA), <0.33 under-expressed in BA)

Affy ID	Gene Name	Fold Change	P-value
65173_at	Cluster Incl. H92987.yv07d04.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-242023 /clone_end=3' /gb=H92987 /gi=1099315 /ug=Hs.13299 /len=650'	0.225358214	0.000567
60058_at	Cluster Incl. AA557237.nl75d07.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1056493 /clone_end=3' /gb=AA557237 /gi=2327714 /ug=Hs.168776 /len=605'	0.224424263	0.021308
56677_at	Cluster Incl. AA557324.nl81a02.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1057034 /clone_end=3' /gb=AA557324 /gi=2327801 /ug=Hs.26040 /len=568'	0.220198572	0.002338
64357_at	Cluster Incl. A1991817.wr32f11.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2489421 /clone_end=3' /gb=A1991817 /gi=5838722 /ug=Hs.237718 /len=388'	0.220156505	0.012518
60532_at	Cluster Incl. AA034289.zk18e07.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-470916 /clone_end=5' /gb=AA034289 /gi=1506098 /ug=Hs.200499 /len=588'	0.219583921	0.006195
58504_at	Cluster Incl. AA149860.zi47e11.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-505100 /clone_end=5' /gb=AA149860 /gi=1720940 /ug=Hs.107755 /len=659'	0.218848321	0.000376
63567_at	Cluster Incl. H50153.yo27e01.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-179160 /clone_end=5' /gb=H50153 /gi=989994 /ug=Hs.21659 /len=580'	0.21856838	0.000001
64137_at	Cluster Incl. A1094860.qa09a11.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1686236 /clone_end=3' /gb=A1094860 /gi=3433836 /ug=Hs.239512 /len=452'	0.217551174	0.005466
58086_i a	Cluster Incl. AA815371.ai64g06.s1 Homo sapiens cDNA, 3 end /clone=1375642 /clone_end=3' /gb=AA815371 /gi=2884967 /ug=Hs.122965 /len=426'	0.216986503	0.000395
62562_at	Cluster Incl. A1674123.wd18d08.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2328495 /clone_end=3' /gb=A1674123 /gi=4874603 /ug=Hs.7615 /len=547'	0.215616168	0.000068
58404_at	Cluster Incl. AA487503.aa95c01.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-839040 /clone_end=3' /gb=AA487503 /gi=2217667 /ug=Hs.100636 /len=486'	0.214993271	0.000121
57792_at	Cluster Incl. AA399630.zi93d07.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-729901 /clone_end=3' /gb=AA399630 /gi=2052644 /ug=Hs.94396 /len=553'	0.213130496	0.000122
62599_r a	Cluster Incl. A1742422.wg40f11.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2367597 /clone_end=3' /gb=A1742422 /gi=5110710 /ug=Hs.174363 /len=577'	0.209883294	0.000954
65165_at	Cluster Incl. A1453545.tj57c03.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2145604 /clone_end=3' /gb=A1453545 /gi=4282767 /ug=Hs.12842 /len=636'	0.20820513	0.011588

Table 4. U95_C Fold Change Genes (>3 over-expressed in Barrett's associated esophageal adenocarcinoma (BA), <0.33 under-expressed in BA)

Affy ID	Gene Name	Fold Change	P-value
64709_at	Cluster Incl. AI810632:tu19b06.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2251475 /clone_end=3' /gb=AI810632 /gi=5397198 /ug=Hs.55080 /len=542'	0.20784757	0
61625_at	Cluster Incl. AI278995:qm22e01.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1882584 /clone_end=3' /gb=AI278995 /gi=3917229 /ug=Hs.27457 /len=581'	0.20742973	0.000095
60445_at	Cluster Incl. AA534542:nf77a03.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-925900 /clone_end=3' /gb=AA534542 /gi=2278795 /ug=Hs.172849 /len=489'	0.206277647	0.015576
49068_at	Cluster Incl. AI031674:ow48g03.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1650100 /clone_end=3' /gb=AI031674 /gi=3249886 /ug=Hs.5850 /len=804'	0.204781876	0.000281
59911_f_a	Cluster Incl. AI124631:am59f08.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1539879 /clone_end=3' /gb=AI124631 /gi=3593145 /ug=Hs.130893 /len=416'	0.202857127	0.034818
53313_at	Cluster Incl. AA284232:zc39c01.T7 Homo sapiens cDNA, 3 end /clone=IMAGE-324672 /clone_end=3' /gb=AA284232 /gi=1928532 /ug=Hs.55983 /len=546'	0.202265466	0.000233
62763_at	Cluster Incl. AI978918:wr61h01.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2492209 /clone_end=3' /gb=AI978918 /gi=5803948 /ug=Hs.179608 /len=588'	0.200697429	0.000276
54326_at	Cluster Incl. AI928203:wo95d03.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2463077 /clone_end=3' /gb=AI928203 /gi=5664167 /ug=Hs.86379 /len=554'	0.196029076	0.000171
48857_at	Cluster Incl. AI924323:wn55d07.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2449357 /clone_end=3' /gb=AI924323 /gi=5660287 /ug=Hs.110024 /len=525'	0.194383948	0.000252
62593_at	Cluster Incl. AA425714:zv47e06.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-756802 /clone_end=5' /gb=AA425714 /gi=2107364 /ug=Hs.173704 /len=454'	0.194165766	0.000008
55676_r_a	Cluster Incl. H40497:yn87f03.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-175421 /clone_end=3' /gb=H40497 /gi=916549 /ug=Hs.237249 /len=446'	0.193742511	0.000159
65550_at	Cluster Incl. AI546943:PN2.1_10_E06.r Homo sapiens cDNA, 5 end /clone_end=5' /gb=AI546943 /gi=4464431 /ug=Hs.23136 /len=706'	0.19337696	0.000005
55581_at	Cluster Incl. AI051688:oy97e02.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1673786 /clone_end=3' /gb=AI051688 /gi=3307222 /ug=Hs.230273 /len=449'	0.192450405	0.035989
60401_at	Cluster Incl. AI769290:wg36b12.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2367167 /clone_end=3' /gb=AI769290 /gi=5235799 /ug=Hs.134190 /len=486'	0.191038508	0.000043

Table 4. U95_C Fold Change Genes (>3 over-expressed in Barrett's associated esophageal adenocarcinoma (BA), <0.33 under-expressed in BA)

Affy ID	Gene Name	Fold Change	P-value
56691_at	Cluster Incl. A1935202:wp17a11.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2465084 /clone_end=3' /gb=A1935202 /gi=5674072 /ug=Hs.31181 /len=571'	0.181080399	0.002371
63476_at	Cluster Incl. A1796235:wh44c01.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2383584 /clone_end=3' /gb=A1796235 /gi=5361687 /ug=Hs.21299 /len=530'	0.179038438	0.000039
53810_f_a	Cluster Incl. AA401302:zv66h05.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-758649 /clone_end=3' /gb=AA401302 /gi=2055205 /ug=Hs.79881 /len=543'	0.175285063	0.000001
65876_at	Cluster Incl. R45447:y943b01.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-35226 /clone_end=3' /gb=R45447 /gi=820704 /ug=Hs.4213 /len=537'	0.168282876	0.001526
50938_at	Cluster Incl. AA778522:af85g10.s1 Homo sapiens cDNA, 3 end /clone=1048866 /clone_end=3' /gb=AA778522 /gi=2837853 /ug=Hs.233824 /len=499'	0.168035248	0.016005
64151_r_a	Cluster Incl. H23482:ym57d12.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-52543 /clone_end=3' /gb=H23482 /gi=892177 /ug=Hs.24088 /len=560'	0.16558005	0.001158
58065_at	Cluster Incl. A1765978:wj23a01.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2403624 /clone_end=3' /gb=A1765978 /gi=5232487 /ug=Hs.122909 /len=338'	0.165471752	0
62968_at	Cluster Incl. A1290476:qj98b08.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1880343 /clone_end=3' /gb=A1290476 /gi=3933250 /ug=Hs.87597 /len=491'	0.161962046	0.010789
61929_at	Cluster Incl. AW024884:gu5878414 /ug=Hs.134478 /len=472'	0.15832857	0.018434
64925_at	Cluster Incl. A1307808:tb28d05.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2055657 /clone_end=3' /gb=A1307808 /gi=4002412 /ug=Hs.7402 /len=622'	0.158241319	0.001113
49042_at	Cluster Incl. AA402161 /gi=2056126 /ug=Hs.239890 /len=540'	0.156140952	0.000036
61681_at	Cluster Incl. AA921922 /gi=3069231 /ug=Hs.31412 /len=488'	0.147708822	0.012553
62723_r_a	Cluster Incl. A1590722:tw87h05.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2266713 /clone_end=3' /gb=A1590722 /gi=4599770 /ug=Hs.167569 /len=691'	0.137146209	0.014933
62817_at	Cluster Incl. A1201812:qj42c12.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1859158 /clone_end=3' /gb=A1201812 /gi=3754418 /ug=Hs.148587 /len=464'	0.13454914	0.007808

Table 4. U95_C Fold Change Genes (>3 over-expressed in Barrett's associated esophageal adenocarcinoma (BA), <0.33 under-expressed in BA)

Affy ID	Gene Name	Fold Change	P-value
63131_i_a	Cluster Incl. R11248:yf41c02.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-129410 /clone_end=5' /gb=R11248 /gi=763983 /ug=Hs.191935 /len=456'	0.133193785	0.00248
60231_at	Cluster Incl. W20054:zb40a08.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-306038 /clone_end=5' /gb=W20054 /gi=1295925 /ug=Hs.102987 /len=574'	0.128912912	0.00004
63059_r_a	Cluster Incl. T79615:yd71e05.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-113696 /clone_end=3' /gb=T79615 /gi=698124 /ug=Hs.184260 /len=569'	0.109126683	0.000031
54320_at	Cluster Incl. A1962905:wf24f04.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2508415 /clone_end=3' /gb=A1962905 /gi=5755618 /ug=Hs.86030 /len=617'	0.103706856	0
61755_i_a	Cluster Incl. W67816:zd38a02.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-342890 /clone_end=5' /gb=W67816 /gi=1376706 /ug=Hs.110196 /len=599'	0.098989494	0.012557
51794_at	Cluster Incl. A1971202:wr26d09.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2488817 /clone_end=3' /gb=A1971202 /gi=5768028 /ug=Hs.239290 /len=587'	0.082261318	0.000014
65618_at	Cluster Incl. A1672527:wb32c06.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2307370 /clone_end=3' /gb=A1672527 /gi=4852258 /ug=Hs.27836 /len=529'	0.078251936	0.000052
62998_at	Cluster Incl. A1831452:wf49b03.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2406125 /clone_end=3' /gb=A1831452 /gi=5452123 /ug=Hs.91539 /len=597'	0.07541159	0.004277
57186_at	Cluster Incl. A1979134:wr70h09.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2493089 /clone_end=3' /gb=A1979134 /gi=5804164 /ug=Hs.230154 /len=494'	0.073273444	0.000306
60228_at	Cluster Incl. R24011:yh29e05.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-131168 /clone_end=5' /gb=R24011 /gi=778899 /ug=Hs.100931 /len=456'	0.059028357	0.000122
54791_at	Cluster Incl. A1620463:tu56a09.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2255032 /clone_end=3' /gb=A1620463 /gi=4629589 /ug=Hs.99197 /len=468'	0.057352223	0.000062
60587_at	Cluster Incl. A1694073:wc82e02.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2325146 /clone_end=3' /gb=A1694073 /gi=4971413 /ug=Hs.48956 /len=443'	0.052183792	0.00012
54805_at	Cluster Incl. A1623978:ts25b06.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2229587 /clone_end=3' /gb=A1623978 /gi=4648909 /ug=Hs.99384 /len=461'	0.04331356	0.000001
62247_at	Cluster Incl. W68630:zd36c11.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-342740 /clone_end=3' /gb=W68630 /gi=1377499 /ug=Hs.161566 /len=510'	0.035040967	0.000179

Table 4. U95_C Fold Change Genes (>3 over-expressed in Barrett's associated esophageal adenocarcinoma (BA), <0.33 under-expressed in BA)

Affy ID	Gene Name	Fold Change	P-value
66443_at	Cluster Incl. AA775536:zf23h10.s1 Homo sapiens cDNA, 3 end /clone=377827 /clone_end=3' /gb=AA775536 /gi=2834870 /ug=Hs.121824 /len=368'	0.032947258	0.000713
61756_r_a	Cluster Incl. W67816:zd38a02.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-342890 /clone_end=5' /gb=W67816 /gi=1376706 /ug=Hs.110196 /len=599'	0.024870079	0.002205
66392_at	Cluster Incl. AA743820:ny29f11.s1 Homo sapiens cDNA /clone=IMAGE-1273197 /gb=AA743820 /gi=2783171 /ug=Hs.120606 /len=466	0.020219012	0.000042

Table 5. U95_D Fold Change Genes (>3 over-expressed in Barrett's associated esophageal adenocarcinoma (BA), <0.33 under-expressed in BA)

Affy ID	Gene Name	Fold Change	P-value
72629_at	Cluster Incl. AI308063:tb22f06.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2055107 /clone_end=3' /gb=AI308063 /gi=4002698 /ug=Hs.222212 /len=205'	126.8832056	0.000003
89917_at	Cluster Incl. AW005911:wz9g01.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2566128 /clone_end=3' /gb=AW005911 /gi=5854701 /ug=Hs.234064 /len=485'	33.92289597	0.000005
86031_at	Cluster Incl. AI803868:tp36g05.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2189912 /clone_end=3' /gb=AI803868 /gi=5369329 /ug=Hs.177164 /len=274'	18.75245815	0.001902
89895_f_a	Cluster Incl. AW001128:wu24f06.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-990870 /clone_end=3' /gb=AW001128 /gi=5848044 /ug=Hs.233945 /len=239'	17.33803078	0.000302
74815_at	Cluster Incl. AI864016:wj53h10.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2406595 /clone_end=3' /gb=AI864016 /gi=5528123 /ug=Hs.234375 /len=511'	17.16521833	0.002611
90481_at	Cluster Incl. AI125252:qd87h06.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1736507 /clone_end=3' /gb=AI125252 /gi=3593766 /ug=Hs.126419 /len=466'	15.90611723	0.000001
77946_at	Cluster Incl. AI744130:wc36f07.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2317285 /clone_end=3' /gb=AI744130 /gi=5112418 /ug=Hs.131201 /len=483'	14.72840034	0.00036
78668_r_a	Cluster Incl. AI673818:to73f12.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2183951 /clone_end=3' /gb=AI673818 /gi=4853549 /ug=Hs.134665 /len=201'	14.66402976	0.003391
73337_at	Cluster Incl. AI355709:qt56h08.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1952031 /clone_end=3' /gb=AI355709 /gi=4095862 /ug=Hs.225823 /len=460'	12.24921906	0.001589
73859_at	Cluster Incl. AW008822:ws71h07.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2502685 /clone_end=3' /gb=AW008822 /gi=5857600 /ug=Hs.231934 /len=369'	12.03887849	0.000945
74904_at	Cluster Incl. AI984156:wu21d07.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-990944 /clone_end=3' /gb=AI984156 /gi=5811375 /ug=Hs.235120 /len=436'	11.93939119	0.000234
85022_at	Cluster Incl. AI039701:ox32g01.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1658064 /clone_end=3' /gb=AI039701 /gi=3278895 /ug=Hs.167408 /len=447'	10.15512075	0.000008
74036_at	Cluster Incl. AW015189:UJ-H-BI0p-aba-c-08-0-UI.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-2711054 /clone_end=3' /gb=AW015189 /gi=5863876 /ug=Hs.232065 /len=407'	9.081911797	0.010398

Table 5. U95_D Fold Change Genes (>3 over-expressed in Barrett's associated esophageal adenocarcinoma (BA), <0.33 under-expressed in BA)

Affy ID	Gene Name	Fold Change	P-value
87776_at	Cluster Incl. AI023610:ov80c08.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1643630 /clone_end=3' /gb=AI023610 /gi=3238654 /ug=Hs.190586 /len=436'	8.799715822	0.000913
82342_at	Cluster Incl. AI675419:wb99b08.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2313783 /clone_end=3' /gb=AI675419 /gi=4875899 /ug=Hs.164464 /len=504'	7.772438703	0.014188
83665_at	Cluster Incl. AI375018:ta54d05.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2047881 /clone_end=3' /gb=AI375018 /gi=4175008 /ug=Hs.158717 /len=474'	7.219466585	0.005004
71502_at	Cluster Incl. AI910824:wi45g06.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2393242 /clone_end=3' /gb=AI910824 /gi=5630560 /ug=Hs.214202 /len=235'	7.213872979	0.000034
71136_at	Cluster Incl. AA631215:nq80g07.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1158684 /clone_end=3' /gb=AA631215 /gi=2553826 /ug=Hs.212640 /len=491'	7.099901302	0.001724
83222_at	Cluster Incl. AA911052:ok65e02.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1518842 /clone_end=3' /gb=AA911052 /gi=3050342 /ug=Hs.174950 /len=451'	7.077863313	0.005694
69494_at	Cluster Incl. AI703451:we24d06.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2342027 /clone_end=3' /gb=AI703451 /gi=4991351 /ug=Hs.202656 /len=433'	6.987691644	0.005066
70836_i a	Cluster Incl. AI824055:wj35e12.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2404846 /clone_end=3' /gb=AI824055 /gi=5444726 /ug=Hs.211396 /len=577'	6.70015517	0.003057
74989_at	Cluster Incl. AW007442:wt55g06.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2511418 /clone_end=3' /gb=AW007442 /gi=5856220 /ug=Hs.235961 /len=424'	6.403445233	0.000249
74767_at	Cluster Incl. AI869919:we75h03.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2346965 /clone_end=3' /gb=AI869919 /gi=5543887 /ug=Hs.234197 /len=279'	6.279662141	0.000435
76918_at	Cluster Incl. AI732969:oh70b01.x5 Homo sapiens cDNA, 3 end /clone=IMAGE-1472329 /clone_end=3' /gb=AI732969 /gi=5054082 /ug=Hs.126245 /len=536'	6.121303029	0.002211
74336_at	Cluster Incl. AW026718:vv44b03.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-990720 /clone_end=3' /gb=AW026718 /gi=5880171 /ug=Hs.233303 /len=693'	5.852600413	0.003442
79398_at	Cluster Incl. AA580664:nd41b07.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-802837 /clone_end=5' /gb=AA580664 /gi=2358321 /ug=Hs.142944 /len=488'	5.528854288	0.013039
81693_at	Cluster Incl. AI582751:tn17b08.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2167863 /clone_end=3' /gb=AI582751 /gi=4568648 /ug=Hs.159028 /len=416'	5.400844754	0.003535

Table 5. U95_D Fold Change Genes (>3 over-expressed in Barrett's associated esophageal adenocarcinoma (BA), <0.33 under-expressed in BA)

Affy ID	Gene Name	Fold Change	P-value
76515_at	Cluster Incl. AA777011:zf28a12.s1 Homo sapiens cDNA, 3 end /clone=378238 /clone_end=3' /gb=AA777011 /gi=2836342 /ug=Hs.122678 /len=485'	5.2764043	0.000093
74689_at	Cluster Incl. AW003135:wq63a10.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2475930 /clone_end=3' /gb=AW003135 /gi=5850051 /ug=Hs.234003 /len=416'	5.204740505	0.017468
89483_i_a	Cluster Incl. AI804066:tc60h05.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2069049 /clone_end=3' /gb=AI804066 /gi=5369538 /ug=Hs.210477 /len=300'	5.160756744	0.000671
80829_at	Cluster Incl. AA210905:zf90h02.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-682995 /clone_end=5' /gb=AA210905 /gi=1809551 /ug=Hs.151875 /len=588'	5.152266697	0.002582
81411_at	Cluster Incl. AI339743:qq42g10.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1935234 /clone_end=3' /gb=AI339743 /gi=4076670 /ug=Hs.157177 /len=476'	5.081809717	0.000737
75224_s	Cluster Incl. AI992172:wt75a05.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2513312 /clone_end=3' /gb=AI992172 /gi=5839077 /ug=Hs.237455 /len=762'	5.038001155	0.000025
81496_at	Cluster Incl. AI870708:wl47h10.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2428099 /clone_end=3' /gb=AI870708 /gi=5544676 /ug=Hs.157601 /len=398'	5.031768797	0.000144
75258_f_a	Cluster Incl. AA224344:zf16d12.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-663575 /clone_end=3' /gb=AA224344 /gi=1844967 /ug=Hs.237937 /len=420'	5.018648158	0.002285
75017_r_a	Cluster Incl. AW006583:wr25f01.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2488729 /clone_end=3' /gb=AW006583 /gi=5855361 /ug=Hs.236125 /len=124'	5.01502499	0.000541
73095_at	Cluster Incl. AI335277:tb29h06.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2055803 /clone_end=3' /gb=AI335277 /gi=4072204 /ug=Hs.224764 /len=388'	4.940911102	0.001852
77486_at	Cluster Incl. AA976712:qq6d04.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1585543 /clone_end=3' /gb=AA976712 /gi=3154158 /ug=Hs.128899 /len=463'	4.920359602	0.022545
87087_at	Cluster Incl. AI283643:qj67c11.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1864532 /clone_end=3' /gb=AI283643 /gi=3921876 /ug=Hs.188120 /len=447'	4.810346144	0.008358
73385_at	Cluster Incl. AA252082:zf63f09.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-668105 /clone_end=3' /gb=AA252082 /gi=1887043 /ug=Hs.226391 /len=399'	4.801518841	0.000861
84678_i_a	Cluster Incl. AI056542:oy98c12.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1673878 /clone_end=3' /gb=AI056542 /gi=3330408 /ug=Hs.164276 /len=361'	4.720912558	0.002732

Table 5. U95_D Fold Change Genes (>3 over-expressed in Barrett's associated esophageal adenocarcinoma (BA), <0.33 under-expressed in BA)

Affy ID	Gene Name	Fold Change	P-value
75737_g	Cluster Incl. AA625990:zu92h03.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-745493 /clone_end=3' /gb=AA625990 /gi=2538377 /ug=Hs.116114 /len=432'	4.719254539	0.004595
77706_at	Cluster Incl. AA641972:ns18f01.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-1183993 /clone_end=5' /gb=AA641972 /gi=2567190 /ug=Hs.130058 /len=447'	4.716780979	0.009315
75242_f_a	Cluster Incl. AW001140:wu24g09.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-990899 /clone_end=3' /gb=AW001140 /gi=5848056 /ug=Hs.237782 /len=415'	4.701250066	0.011085
84996_at	Cluster Incl. AI379186:tc66d08.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2069583 /clone_end=3' /gb=AI379186 /gi=4189039 /ug=Hs.167183 /len=473'	4.6838985	0.001649
90289_at	Cluster Incl. AI827330:w10d06.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2424491 /clone_end=3' /gb=AI827330 /gi=5448001 /ug=Hs.120750 /len=435'	4.653039196	0.014564
78672_at	Cluster Incl. AI276246:ql65e01.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1877208 /clone_end=3' /gb=AI276246 /gi=3898520 /ug=Hs.134702 /len=473'	4.623270914	0.000543
77739_i_a	Cluster Incl. AA910562:ok66g12.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1518982 /clone_end=3' /gb=AA910562 /gi=3049852 /ug=Hs.130207 /len=416'	4.589575228	0.00161
89820_at	Cluster Incl. AI828439:wk85b01.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2422153 /clone_end=3' /gb=AI828439 /gi=5449110 /ug=Hs.231580 /len=388'	4.574990842	0.016532
80876_at	Cluster Incl. AA513406:ne59g08.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-901694 /clone_end=3' /gb=AA513406 /gi=2251818 /ug=Hs.152307 /len=467'	4.547281772	0.019458
83883_at	Cluster Incl. AA927837:on79e06.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1562914 /clone_end=3' /gb=AA927837 /gi=3077127 /ug=Hs.160112 /len=348'	4.503173747	0.011657
74077_at	Cluster Incl. AA888985:ak24f07.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1406917 /clone_end=3' /gb=AA888985 /gi=3015855 /ug=Hs.232115 /len=369'	4.464473172	0.004661
92121_r_a	Cluster Incl. AI022636:ox05f02.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1655451 /clone_end=3' /gb=AI022636 /gi=3237877 /ug=Hs.175531 /len=495'	4.380454753	0.045704
80193_at	Cluster Incl. AI130878:qc14d09.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1709585 /clone_end=3' /gb=AI130878 /gi=3600894 /ug=Hs.146517 /len=432'	4.312572045	0.005574
70825_at	Cluster Incl. AI301513:qr44h05.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1901145 /clone_end=3' /gb=AI301513 /gi=3960859 /ug=Hs.211386 /len=427'	4.257879375	0.000701

Table 5. U95_D Fold Change Genes (>3 over-expressed in Barrett's associated esophageal adenocarcinoma (BA), <0.33 under-expressed in BA)

Affy ID	Gene Name	Fold Change	P-value
78478_r_a	Cluster Incl. H89231: yw25g04.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-253302 /clone_end=5' /gb=H89231 /gi=1071491 /ug=Hs.133504 /len=395'	4.235271418	0.004183
90910_at	Cluster Incl. A1091388: oo26f02.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1567323 /clone_end=3' /gb=A1091388 /gi=3430447 /ug=Hs.134855 /len=485'	4.208360659	0.005383
81303_at	Cluster Incl. A1346656: qp52b03.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1926605 /clone_end=3' /gb=A1346656 /gi=4083862 /ug=Hs.156652 /len=585'	4.20318803	0.031305
82896_at	Cluster Incl. A1476732: tm23f10.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2157451 /clone_end=3' /gb=A1476732 /gi=4329777 /ug=Hs.170624 /len=446'	4.169388472	0.037823
87624_at	Cluster Incl. AA668464: ab86a05.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-853808 /clone_end=3' /gb=AA668464 /gi=2629963 /ug=Hs.190309 /len=328'	4.167316157	0.002637
91225_at	Cluster Incl. AW015211: UI-H-B10p-aba-e-11-0-UI.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-2711156 /clone_end=3' /gb=AW015211 /gi=5863898 /ug=Hs.146181 /len=471'	4.164345384	0.00008
81939_at	Cluster Incl. A1417773: th31c01.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2119872 /clone_end=3' /gb=A1417773 /gi=4261277 /ug=Hs.161145 /len=382'	4.138057591	0.004722
69357_at	Cluster Incl. A1753726: cr14c07.x1 Homo sapiens cDNA, 3 end /clone=HBMSC_cr14c07 /clone_end=3' /gb=A1753726 /gi=5131990 /ug=Hs.202333 /len=449'	4.130344884	0.001956
77353_at	Cluster Incl. A1733279: oo46f12.x5 Homo sapiens cDNA, 3 end /clone=IMAGE-1569263 /clone_end=3' /gb=A1733279 /gi=5054392 /ug=Hs.128317 /len=271'	4.121422229	0.008861
79696_at	Cluster Incl. AA013440: ze26e09.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-360136 /clone_end=3' /gb=AA013440 /gi=1474486 /ug=Hs.144252 /len=463'	4.09631447	0.012229
86510_at	Cluster Incl. A1076326: oy95d08.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1673583 /clone_end=3' /gb=A1076326 /gi=3405504 /ug=Hs.185677 /len=441'	4.086715666	0.025182
79369_at	Cluster Incl. AA927001: om26d10.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1542163 /clone_end=3' /gb=AA927001 /gi=3075898 /ug=Hs.142584 /len=346'	4.051608302	0.000344
88942_at	Cluster Incl. A1300447: qo13f06.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1908419 /clone_end=3' /gb=A1300447 /gi=3959793 /ug=Hs.202429 /len=327'	4.040588934	0.013394
84125_at	Cluster Incl. R86170: yp88e07.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-194532 /clone_end=5' /gb=R86170 /gi=944576 /ug=Hs.161221 /len=467'	4.014774285	0.00934

Table 5. U95_D Fold Change Genes (>3 over-expressed in Barrett's associated esophageal adenocarcinoma (BA), <0.33 under-expressed in BA)

Affy ID	Gene Name	Fold Change	P-value
73210_at	Cluster Incl. A1872472:ty42e07.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2281764 /clone_end=3' /gb=A1872472 /gi=5546521 /ug=Hs.225040 /len=401'	4.008599635	0.001324
76569_at	Cluster Incl. A1700684:we39c12.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2343478 /clone_end=3' /gb=A1700684 /gi=4988584 /ug=Hs.134166 /len=571'	4.002473204	0.000006
77117_at	Cluster Incl. AA938245:oo95b09.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1573913 /clone_end=3' /gb=AA938245 /gi=3096356 /ug=Hs.127160 /len=421'	3.972806977	0.012473
70838_r_a	Cluster Incl. A1824055:wj35e12.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2404846 /clone_end=3' /gb=A1824055 /gi=5444726 /ug=Hs.211396 /len=577'	3.946917752	0.023713
91676_at	Cluster Incl. AA534325:nf75e10.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-925770 /clone_end=3' /gb=AA534325 /gi=2278578 /ug=Hs.162183 /len=460'	3.926181357	0.019084
68192_at	Cluster Incl. T92888:ye22e09.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-118504 /clone_end=3' /gb=T92888 /gi=724801 /ug=Hs.191864 /len=495'	3.901616313	0.014332
84978_at	Cluster Incl. A1362920:qy81c11.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2018420 /clone_end=3' /gb=A1362920 /gi=4114541 /ug=Hs.167139 /len=388'	3.879227403	0.03697
82314_at	Cluster Incl. A1436813:th82h12.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2125223 /clone_end=3' /gb=A1436813 /gi=4284696 /ug=Hs.164217 /len=508'	3.836361251	0.02183
82070_at	Cluster Incl. AA564641:jl=2336280 /ug=Hs.162343 /len=475'	3.77142292	0.003544
79351_at	Cluster Incl. AA195514:jl=1785400 /ug=Hs.142104 /len=385'	3.764326148	0.04421
84289_at	Cluster Incl. A1912393:tz05a01.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2287656 /clone_end=3' /gb=A1912393 /gi=5632248 /ug=Hs.162279 /len=454'	3.732611335	0.00756
70936_at	Cluster Incl. A1921300:wo23a09.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2456152 /clone_end=3' /gb=A1921300 /gi=5657264 /ug=Hs.211711 /len=613'	3.728217248	0.019033
74810_s	Cluster Incl. AW021074:df18e02.y1 Homo sapiens cDNA, 5 end /clone=IMAGE-2483787 /clone_end=5' /gb=AW021074 /gi=5874604 /ug=Hs.234355 /len=351'	3.722045457	0.00037
75014_i_a	Cluster Incl. AW006583:wr25f01.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2488729 /clone_end=3' /gb=AW006583 /gi=5855361 /ug=Hs.236125 /len=124'	3.681403454	0.000484

Table 5. U95_D Fold Change Genes (>3 over-expressed in Barrett's associated esophageal adenocarcinoma (BA), <0.33 under-expressed in BA)

Affy ID	Gene Name	Fold Change	P-value
77741_r_a	Cluster Incl. AA910562:ok66g12.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1518982 /clone_end=3' /gb=AA910562 /gi=3049852 /ug=Hs.130207 /len=416'	3.68077061	0.004724
78304_at	Cluster Incl. AI056977:oy89d09.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1673009 /clone_end=3' /gb=AI056977 /gi=3330766 /ug=Hs.132900 /len=459'	3.617156362	0.013155
80124_at	Cluster Incl. AA643238:nr61f06.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1172483 /clone_end=3' /gb=AA643238 /gi=2568456 /ug=Hs.146144 /len=476'	3.580942752	0.001471
84304_at	Cluster Incl. AA521177:aa73f03.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-826589 /clone_end=3' /gb=AA521177 /gi=2261720 /ug=Hs.162409 /len=559'	3.57711283	0.002455
89972_at	Cluster Incl. AI420969:te97b09.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2094617 /clone_end=3' /gb=AI420969 /gi=4266900 /ug=Hs.235870 /len=383'	3.575423765	0.007712
90581_at	Cluster Incl. AA974579:op28g10.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1578210 /clone_end=3' /gb=AA974579 /gi=3149759 /ug=Hs.128385 /len=408'	3.567570093	0.028452
74922_at	Cluster Incl. AW025554:wu97g07.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-990991 /clone_end=3' /gb=AW025554 /gi=5879084 /ug=Hs.235239 /len=443'	3.544362859	0.008025
81319_at	Cluster Incl. AI686894:tp90h06.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2206619 /clone_end=3' /gb=AI686894 /gi=4898188 /ug=Hs.156704 /len=476'	3.538203629	0.01427
88620_at	Cluster Incl. AI970185:wr08c07.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2480940 /clone_end=3' /gb=AI970185 /gi=5767011 /ug=Hs.197641 /len=514'	3.533373724	0.00708
87615_r_a	Cluster Incl. AA626219:zv88a11.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-766844 /clone_end=3' /gb=AA626219 /gi=2538606 /ug=Hs.190274 /len=263'	3.515678463	0.030307
77005_r_a	Cluster Incl. AA918616:ol67a12.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1534654 /clone_end=3' /gb=AA918616 /gi=3058506 /ug=Hs.126658 /len=495'	3.50824968	0.004026
81874_at	Cluster Incl. AI734974:as54e06.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2332546 /clone_end=3' /gb=AI734974 /gi=5056498 /ug=Hs.160604 /len=506'	3.495899557	0.042114
90190_at	Cluster Incl. AI819924:wj11c04.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2402502 /clone_end=3' /gb=AI819924 /gi=5439003 /ug=Hs.116559 /len=534'	3.492860427	0.000238
88949_at	Cluster Incl. AI744009:wc32f04.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2316895 /clone_end=3' /gb=AI744009 /gi=5112297 /ug=Hs.202451 /len=568'	3.484438351	0.000883

Table 5. U95_D Fold Change Genes (>3 over-expressed in Barrett's associated esophageal adenocarcinoma (BA), <0.33 under-expressed in BA)

Affy ID	Gene Name	Fold Change	P-value
92039_at	Cluster Incl. AI955491:wt30e12.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2509006 /clone_end=3' /gb=AI955491 /gi=5747801 /ug=Hs.171372 /len=671'	3.436563997	0.006207
74868_at	Cluster Incl. AI991048:wu36c07.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-990847 /clone_end=3' /gb=AI991048 /gi=5837945 /ug=Hs.234668 /len=429'	3.42763578	0.000285
85706_at	Cluster Incl. AI218358:qh21g07.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1845372 /clone_end=3' /gb=AI218358 /gi=3798173 /ug=Hs.175048 /len=411'	3.422351762	0.017153
71117_f_a	Cluster Incl. AI982832:wt44e02.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2510330 /clone_end=3' /gb=AI982832 /gi=5810051 /ug=Hs.212529 /len=497'	3.418516359	0.001844
68339_at	Cluster Incl. AI624028:ts25g07.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2229660 /clone_end=3' /gb=AI624028 /gi=4648959 /ug=Hs.192626 /len=213'	3.404452919	0.000617
78680_at	Cluster Incl. AA282171:zf02c06.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-711946 /clone_end=3' /gb=AA282171 /gi=1925032 /ug=Hs.134740 /len=427'	3.401834363	0.009019
90436_at	Cluster Incl. W93113:zh45f06.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-415043 /clone_end=3' /gb=W93113 /gi=1422275 /ug=Hs.125212 /len=421'	3.40090527	0.021093
81650_at	Cluster Incl. AA631047:nq77b01.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1158313 /clone_end=3' /gb=AA631047 /gi=2553658 /ug=Hs.158761 /len=588'	3.353588529	0.000357
73248_at	Cluster Incl. AI955755:wt59b10.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2511739 /clone_end=3' /gb=AI955755 /gi=5748065 /ug=Hs.225142 /len=525'	3.33387584	0.006207
73315_at	Cluster Incl. AI868289:tf44g02.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2144402 /clone_end=3' /gb=AI868289 /gi=5541305 /ug=Hs.225651 /len=289'	3.332728736	0.00066
67401_at	Cluster Incl. AI434675:ti35f10.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2132491 /clone_end=3' /gb=AI434675 /gi=4297838 /ug=Hs.164299 /len=340'	3.330352227	0.00106
76150_at	Cluster Incl. AA778773:zj41h06.s1 Homo sapiens cDNA, 3 end /clone=452891 /clone_end=3' /gb=AA778773 /gi=2838104 /ug=Hs.119691 /len=423'	3.324537689	0.01164
75183_at	Cluster Incl. AI990633:ws22f07.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2497957 /clone_end=3' /gb=AI990633 /gi=5837514 /ug=Hs.237246 /len=445'	3.313399383	0.006284
80971_at	Cluster Incl. AI033377:ox03b10.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1655227 /clone_end=3' /gb=AI033377 /gi=3254330 /ug=Hs.153298 /len=485'	3.307979211	0.008879

Table 5. U95_D Fold Change Genes (>3 over-expressed in Barrett's associated esophageal adenocarcinoma (BA), <0.33 under-expressed in BA)

Affy ID	Gene Name	Fold Change	P-value
86810_at	Cluster Incl. AI581415:to71f12.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2183759 /clone_end=3' /gb=AI581415 /gi=4565791 /ug=Hs.187260 /len=392'	3.286327472	0.027513
80261_s	Cluster Incl. AI961818:wf66g05.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2512472 /clone_end=3' /gb=AI961818 /gi=5754531 /ug=Hs.146916 /len=643'	3.248004767	0.00471
71177_at	Cluster Incl. AI921931:wn86g12.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2452774 /clone_end=3' /gb=AI921931 /gi=5657895 /ug=Hs.212815 /len=516'	3.241857044	0.020963
81927_at	Cluster Incl. AI417669:ig80g11.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2115140 /clone_end=3' /gb=AI417669 /gi=4261173 /ug=Hs.161134 /len=391'	3.235184899	0.038241
80623_s	Cluster Incl. AI640222:wa30f03.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2299613 /clone_end=3' /gb=AI640222 /gi=4703331 /ug=Hs.149993 /len=451'	3.218612679	0.008845
74696_r_a	Cluster Incl. AW003358:wq65g09.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2476192 /clone_end=3' /gb=AW003358 /gi=5850274 /ug=Hs.234010 /len=406'	3.216414783	0.000981
87133_at	Cluster Incl. AI275499:ql74d03.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1878053 /clone_end=3' /gb=AI275499 /gi=3897773 /ug=Hs.188350 /len=472'	3.215553093	0.029742
77363_at	Cluster Incl. AI651606:wb07c02.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2304962 /clone_end=3' /gb=AI651606 /gi=4735585 /ug=Hs.128395 /len=588'	3.205498008	0.0075
75791_f_a	Cluster Incl. AI821102:nr20h03.y5 Homo sapiens cDNA /clone=IMAGE-1168565 /gb=AI821102 /gi=5440181 /ug=Hs.116350 /len=419	3.197729341	0.013912
73261_at	Cluster Incl. AI692539:wd73e11.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2337260 /clone_end=3' /gb=AI692539 /gi=4969879 /ug=Hs.225186 /len=534'	3.194807353	0.000008
81717_at	Cluster Incl. AI375700:ta58g09.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2048320 /clone_end=3' /gb=AI375700 /gi=4175690 /ug=Hs.159185 /len=407'	3.189360956	0.024927
69102_at	Cluster Incl. AI950819:wx55f02.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2547579 /clone_end=3' /gb=AI950819 /gi=5743129 /ug=Hs.201680 /len=484'	3.182469138	0.037281
81452_at	Cluster Incl. AI421933:tf45a12.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2099134 /clone_end=3' /gb=AI421933 /gi=4267864 /ug=Hs.157383 /len=465'	3.159839766	0.024083
83115_at	Cluster Incl. AI346114:qp48f09.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1926281 /clone_end=3' /gb=AI346114 /gi=4083320 /ug=Hs.173495 /len=458'	3.143614459	0.003379

Table 5. U95_D Fold Change Genes (>3 over-expressed in Barrett's associated esophageal adenocarcinoma (BA), <0.33 under-expressed in BA)

Affy ID	Gene Name	Fold Change	P-value
74630_r_a	Cluster Incl. AA995791:os29f07.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1606789 /clone_end=3' /gb=AA995791 /gi=3182280 /ug=Hs.233832 /len=477	3.121958997	0.046206
80664_at	Cluster Incl. AI248671:qh66g01.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1849680 /clone_end=3' /gb=AI248671 /gi=3844068 /ug=Hs.150289 /len=432	3.116104719	0.004129
78136_at	Cluster Incl. AI038623:ox39b12.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1658687 /clone_end=3' /gb=AI038623 /gi=3277817 /ug=Hs.132087 /len=452	3.114649496	0.037841
68888_at	Cluster Incl. AI671829:wb34d12.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2307575 /clone_end=3' /gb=AI671829 /gi=4851560 /ug=Hs.200573 /len=504	3.114197965	0.03414
79683_at	Cluster Incl. AI223034:qg52h05.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1838841 /clone_end=3' /gb=AI223034 /gi=3805237 /ug=Hs.144137 /len=497	3.104715847	0.018458
75012_at	Cluster Incl. AI989698:ws35d09.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2499185 /clone_end=3' /gb=AI989698 /gi=5836579 /ug=Hs.236112 /len=380	3.103880371	0.037238
67147_at	Cluster Incl. AI040048:ox28a08.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1657622 /clone_end=3' /gb=AI040048 /gi=3279242 /ug=Hs.157207 /len=416	3.098224539	0.032493
72075_at	Cluster Incl. AA279019:zs83a10.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-704058 /clone_end=3' /gb=AA279019 /gi=1920638 /ug=Hs.221039 /len=445	3.08870358	0.004529
69524_at	Cluster Incl. AI739558:wi35a05.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2392208 /clone_end=3' /gb=AI739558 /gi=5101539 /ug=Hs.203481 /len=335	3.079273337	0.033429
72512_at	Cluster Incl. AA653151:ag64c01.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1127712 /clone_end=3' /gb=AA653151 /gi=2589322 /ug=Hs.222057 /len=408	3.065825864	0.041772
71211_at	Cluster Incl. AI050877:oy47c06.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1668970 /clone_end=3' /gb=AI050877 /gi=3307682 /ug=Hs.212948 /len=357	3.041281957	0.002806
88788_i_a	Cluster Incl. AA969517:oo85a11.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1572956 /clone_end=3' /gb=AA969517 /gi=3144697 /ug=Hs.201079 /len=377	3.032310778	0.005066
77052_at	Cluster Incl. AI914225:wd74g03.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2337364 /clone_end=3' /gb=AI914225 /gi=5634080 /ug=Hs.126865 /len=447	3.023302076	0.004485
75551_at	Cluster Incl. AI566143:tn53h10.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2172163 /clone_end=3' /gb=AI566143 /gi=4524595 /ug=Hs.113010 /len=420	3.017433674	0.021729

Table 5. U95_D Fold Change Genes (>3 over-expressed in Barrett's associated esophageal adenocarcinoma (BA), <0.33 under-expressed in BA)

Affy ID	Gene Name	Fold Change	P-value
84740_at	Cluster Incl. N73628:yz78b01.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-289129 /clone_end=3' /gb=N73628 /gi=1230913 /ug=Hs.165153 /len=453'	3.014935259	0.020032
74611_s	Cluster Incl. AI983615:wu19h07.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-990800 /clone_end=3' /gb=AI983615 /gi=5810834 /ug=Hs.233756 /len=482'	3.012380075	0.042251
76464_g	Cluster Incl. AA781854:ai61h03.s1 Homo sapiens cDNA, 3 end /clone=1375349 /clone_end=3' /gb=AA781854 /gi=2841185 /ug=Hs.122275 /len=367'	3.006117339	0.0097
90055_s	Cluster Incl. AA778124:zf46g09.s1 Homo sapiens cDNA, 3 end /clone=380032 /clone_end=3' /gb=AA778124 /gi=2837525 /ug=Hs.238767 /len=466'	0.327601885	0.003177
89108_at	Cluster Incl. AA780912:ag98f07.s1 Homo sapiens cDNA, 3 end /clone=1155205 /clone_end=3' /gb=AA780912 /gi=2840243 /ug=Hs.204249 /len=489'	0.326532542	0.031272
78594_at	Cluster Incl. AI080633:ox54b12.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1660127 /clone_end=3' /gb=AI080633 /gi=3416884 /ug=Hs.134225 /len=519'	0.326310174	0.04264
84816_at	Cluster Incl. AA995233:ou17a03.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1626508 /clone_end=3' /gb=AA995233 /gi=3181722 /ug=Hs.166309 /len=497'	0.326189959	0.000316
76410_at	Cluster Incl. H05391:y180b11.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-44222 /clone_end=5' /gb=H05391 /gi=868943 /ug=Hs.122008 /len=443'	0.316419067	0.001262
74367_at	Cluster Incl. AI989468:ws25b02.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2498187 /clone_end=3' /gb=AI989468 /gi=5836349 /ug=Hs.233354 /len=407'	0.315634857	0.005064
88668_at	Cluster Incl. AI631519:wa99a02.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2304266 /clone_end=3' /gb=AI631519 /gi=4682849 /ug=Hs.198000 /len=494'	0.314758398	0.028635
91172_at	Cluster Incl. AA772360:ai43d11.s1 Homo sapiens cDNA, 3 end /clone=1359765 /clone_end=3' /gb=AA772360 /gi=2824143 /ug=Hs.145274 /len=471'	0.31434908	0.013501
80238_at	Cluster Incl. AA507036:ni02h04.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-966871 /clone_end=3' /gb=AA507036 /gi=2243475 /ug=Hs.146822 /len=466'	0.311633699	0.003808
85907_at	Cluster Incl. AI276085:q174f09.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1878089 /clone_end=3' /gb=AI276085 /gi=3898359 /ug=Hs.176222 /len=465'	0.31047302	0.004634
80485_i_a	Cluster Incl. AI808768:wf57h12.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2359751 /clone_end=3' /gb=AI808768 /gi=5395334 /ug=Hs.148867 /len=481'	0.308522904	0.016329

Table 5. U95_D Fold Change Genes (>3 over-expressed in Barrett's associated esophageal adenocarcinoma (BA), <0.33 under-expressed in BA)

Affy ID	Gene Name	Fold Change	P-value
72026_g	Cluster Incl. AA427578:zw54b07.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-773845 /clone_end=3' /gb=AA427578 /gi=2112006 /ug=Hs.220975 /len=525'	0.308401991	0.001714
72703_at	Cluster Incl. AA010008:zi07c10.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-430098 /clone_end=3' /gb=AA010008 /gi=1471055 /ug=Hs.222505 /len=436'	0.307232814	0.000017
87230_at	Cluster Incl. AA521281:aa75g12.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-826822 /clone_end=3' /gb=AA521281 /gi=2261824 /ug=Hs.188830 /len=556'	0.305350897	0.049077
77885_at	Cluster Incl. A1733673:ov09h03.x5 Homo sapiens cDNA, 3 end /clone=IMAGE-1636853 /clone_end=3' /gb=A1733673 /gi=5054786 /ug=Hs.131005 /len=464'	0.305290936	0.00235
87827_at	Cluster Incl. A1200630:qf87g12.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1757062 /clone_end=3' /gb=A1200630 /gi=3753236 /ug=Hs.190725 /len=449'	0.303677717	0.022954
73346_at	Cluster Incl. AA732736:ai28a09.s1 Homo sapiens cDNA, 3 end /clone=1344088 /clone_end=3' /gb=AA732736 /gi=2754095 /ug=Hs.225853 /len=464'	0.303166429	0.000992
76154_i_a	Cluster Incl. A1634548:tx52g01.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2273232 /clone_end=3' /gb=A1634548 /gi=4685878 /ug=Hs.119748 /len=523'	0.302833962	0.000105
79735_at	Cluster Incl. AA037529:zk36c07.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-484908 /clone_end=5' /gb=AA037529 /gi=1512629 /ug=Hs.144559 /len=489'	0.302793001	0.000342
84844_at	Cluster Incl. A1269474:qh47e02.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1847834 /clone_end=3' /gb=A1269474 /gi=3888641 /ug=Hs.166420 /len=398'	0.301592705	0.006328
80874_at	Cluster Incl. A1659898:tu01d09.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2249777 /clone_end=3' /gb=A1659898 /gi=4763468 /ug=Hs.152298 /len=521'	0.299388186	0.014565
84768_at	Cluster Incl. A1446224:ij25f11.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2142573 /clone_end=3' /gb=A1446224 /gi=4293712 /ug=Hs.165817 /len=350'	0.295386963	0.010618
77908_at	Cluster Incl. A1016841:ov33d08.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1639119 /clone_end=3' /gb=A1016841 /gi=3231177 /ug=Hs.131106 /len=408'	0.29124207	0.009569
76248_at	Cluster Incl. A1653732:wb36g02.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2307794 /clone_end=3' /gb=A1653732 /gi=4737711 /ug=Hs.120691 /len=457'	0.288672932	0.038981
75779_at	Cluster Incl. AA629059:zu84b05.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-744657 /clone_end=3' /gb=AA629059 /gi=2541446 /ug=Hs.116298 /len=570'	0.286202318	0.01828

Table 5. U95_D Fold Change Genes (>3 over-expressed in Barrett's associated esophageal adenocarcinoma (BA), <0.33 under-expressed in BA)

Affy ID	Gene Name	Fold Change	P-value
91145_at	Cluster Incl. A1759990:wh36g05.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2382872 /clone_end=3' /gb=A1759990 /gi=5175657 /ug=Hs.144824 /len=351'	0.285672403	0.004773
75293_s	Cluster Incl. AW009667:ws85g02.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2504786 /clone_end=3' /gb=AW009667 /gi=5858445 /ug=Hs.238353 /len=601'	0.284658559	0.003682
81973_r_a	Cluster Incl. A1421200:tf24f09.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2097161 /clone_end=3' /gb=A1421200 /gi=4267131 /ug=Hs.161312 /len=422'	0.284252973	0.010971
AFFX-HU	M33197 Human glyceraldehyde-3-phosphate dehydrogenase (GAPDH) mRNA, complete cds (5, _M, _3 represent transcript regions 5 prime, Middle, and 3 prime respectively)	0.284040649	0.015245
91840_at	Cluster Incl. W39635:zc19c08.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-322766 /clone_end=5' /gb=W39635 /gi=1321344 /ug=Hs.167828 /len=435'	0.282077522	0.038709
83720_at	Cluster Incl. A1380073:tf78f01.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2105401 /clone_end=3' /gb=A1380073 /gi=4189926 /ug=Hs.158949 /len=443'	0.280175516	0.000283
81035_i_a	Cluster Incl. A1573275:tn03f10.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2166571 /clone_end=3' /gb=A1573275 /gi=4536649 /ug=Hs.153892 /len=503'	0.278845944	0.042646
73217_at	Cluster Incl. A1950400:wq35a04.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2473230 /clone_end=3' /gb=A1950400 /gi=5742710 /ug=Hs.225073 /len=684'	0.278037315	0.023478
87996_at	Cluster Incl. A1215886:qm35g06.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1883866 /clone_end=3' /gb=A1215886 /gi=3784927 /ug=Hs.191824 /len=483'	0.271801622	0.027086
69515_at	Cluster Incl. A1738451:w32a06.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2391922 /clone_end=3' /gb=A1738451 /gi=5100432 /ug=Hs.203304 /len=534'	0.26449689	0.003509
79472_at	Cluster Incl. N53442:yy41a09.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-245272 /clone_end=3' /gb=N53442 /gi=1194608 /ug=Hs.143443 /len=479'	0.264444183	0.000068
81629_r_a	Cluster Incl. A1939503:qy19d04.x5 Homo sapiens cDNA, 3 end /clone=IMAGE-2012455 /clone_end=3' /gb=A1939503 /gi=5678292 /ug=Hs.158545 /len=428'	0.26339748	0.000103
92166_at	Cluster Incl. A1190864:qd55a08.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1733366 /clone_end=3' /gb=A1190864 /gi=3742073 /ug=Hs.178226 /len=451'	0.261339615	0.00325
81217_at	Cluster Incl. A1971594:wq87h01.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2479057 /clone_end=3' /gb=A1971594 /gi=5768420 /ug=Hs.156105 /len=501'	0.261004215	0.009305

Table 5. U95_D Fold Change Genes (>3 over-expressed in Barrett's associated esophageal adenocarcinoma (BA), <0.33 under-expressed in BA)

Affy ID	Gene Name	Fold Change	P-value
89937_at	Cluster Incl. AA700625:z43a06.s1 Homo sapiens cDNA, 3 end /clone=433522 /clone_end=3' /gb=AA700625 /gi=2703588 /ug=Hs.234473 /len=564'	0.258257021	0.001392
81584_at	Cluster Incl. A1828498:wk30a12.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2413822 /clone_end=3' /gb=A1828498 /gi=5449169 /ug=Hs.158186 /len=539'	0.257194389	0.016235
70409_at	Cluster Incl. A1792564:q17h09.y5 Homo sapiens cDNA, 5 end /clone=IMAGE-1862177 /clone_end=5' /gb=A1792564 /gi=5340280 /ug=Hs.209447 /len=326'	0.253124275	0.019626
88042_i_a	Cluster Incl. AA704465:z19c02.s1 Homo sapiens cDNA, 3 end /clone=450722 /clone_end=3' /gb=AA704465 /gi=2714383 /ug=Hs.191941 /len=480'	0.252686592	0.000395
74756_at	Cluster Incl. A1869008:wc17h01.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2315473 /clone_end=3' /gb=A1869008 /gi=5542976 /ug=Hs.234184 /len=352'	0.25104725	0.01521
80680_at	Cluster Incl. A1279514:q151c11.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1875860 /clone_end=3' /gb=A1279514 /gi=3917748 /ug=Hs.150459 /len=555'	0.247710917	0.036068
71324_at	Cluster Incl. A1761935:wh50a05.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2384144 /clone_end=3' /gb=A1761935 /gi=5177602 /ug=Hs.213335 /len=452'	0.247617951	0.004563
69100_at	Cluster Incl. A1682297:wc51d01.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2322145 /clone_end=3' /gb=A1682297 /gi=4892479 /ug=Hs.201657 /len=481'	0.247438489	0.001126
82786_at	Cluster Incl. AW014764:U1-H-B10-aae-f-08-O-U1.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-2709254 /clone_end=3' /gb=AW014764 /gi=5863521 /ug=Hs.169169 /len=383'	0.245652038	0.017259
75211_s_	Cluster Incl. H78699:yu29h01.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-235249 /clone_end=3' /gb=H78699 /gi=1056788 /ug=Hs.237375 /len=418'	0.244829232	0.000058
78158_at	Cluster Incl. A1042180:oy37c12.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1668022 /clone_end=3' /gb=A1042180 /gi=3281374 /ug=Hs.132160 /len=533'	0.24479353	0.000431
79294_i_a	Cluster Incl. R95918:yq51f07.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-199333 /clone_end=3' /gb=R95918 /gi=981578 /ug=Hs.140871 /len=296'	0.240319896	0.003866
68112_at	Cluster Incl. AA931562:oo56c11.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1570196 /clone_end=3' /gb=AA931562 /gi=3085948 /ug=Hs.190736 /len=488'	0.240105629	0.029475
79618_at	Cluster Incl. A1740621:wg23e12.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2365966 /clone_end=3' /gb=A1740621 /gi=5108909 /ug=Hs.143873 /len=457'	0.239308307	0.004818

Table 5. U95_D Fold Change Genes (>3 over-expressed in Barrett's associated esophageal adenocarcinoma (BA), <0.33 under-expressed in BA)

Affy ID	Gene Name	Fold Change	P-value
75719_at	Cluster Incl. A1039291:ox33e10.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1658154 /clone_end=3' /gb=A1039291 /gi=3278485 /ug=Hs.116061 /len=435'	0.239047129	0.001528
78779_at	Cluster Incl. A1087874:ow60d03.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1651205 /clone_end=3' /gb=A1087874 /gi=3426907 /ug=Hs.135162 /len=515'	0.238520097	0.003141
71787_r_a	Cluster Incl. A1312358:ta78h12.x2 Homo sapiens cDNA, 3 end /clone=IMAGE-2050247 /clone_end=3' /gb=A1312358 /gi=4017963 /ug=Hs.220599 /len=146'	0.237885742	0.033666
71560_r_a	Cluster Incl. A1932356:wd27d09.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2329361 /clone_end=3' /gb=A1932356 /gi=5671093 /ug=Hs.216016 /len=486'	0.234298993	0.002953
78580_at	Cluster Incl. A1344345:tc03h05.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2062809 /clone_end=3' /gb=A1344345 /gi=4081551 /ug=Hs.134198 /len=501'	0.234044364	0.003148
78563_at	Cluster Incl. A1302188:qn58d06.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1902443 /clone_end=3' /gb=A1302188 /gi=3961534 /ug=Hs.134128 /len=464'	0.228535599	0.000468
87915_i_a	Cluster Incl. W93079:zh45a08.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-414998 /clone_end=3' /gb=W93079 /gi=1422241 /ug=Hs.191396 /len=352'	0.223549654	0.000173
90914_at	Cluster Incl. A1088153:oz96a09.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1683160 /clone_end=3' /gb=A1088153 /gi=3427129 /ug=Hs.134902 /len=485'	0.219235587	0.040539
86791_at	Cluster Incl. AA461106:zx63g09.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-796192 /clone_end=3' /gb=AA461106 /gi=2186226 /ug=Hs.187123 /len=400'	0.218378808	0.000089
89355_at	Cluster Incl. A1819564:wj91f12.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2410223 /clone_end=3' /gb=A1819564 /gi=5438643 /ug=Hs.208230 /len=469'	0.214671449	0.001157
88225_at	Cluster Incl. AA779891:af46d05.s1 Homo sapiens cDNA, 3 end /clone=1034697 /clone_end=3' /gb=AA779891 /gi=2839222 /ug=Hs.193052 /len=472'	0.213518745	0.005318
73771_at	Cluster Incl. A1632232:tt20e05.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2241344 /clone_end=3' /gb=A1632232 /gi=4683562 /ug=Hs.231855 /len=496'	0.212420493	0.002735
82591_r_a	Cluster Incl. A1309223:qo68a10.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1913658 /clone_end=3' /gb=A1309223 /gi=4004094 /ug=Hs.167011 /len=331'	0.212211885	0.006857
80687_at	Cluster Incl. AA921994:om41a07.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1543572 /clone_end=3' /gb=AA921994 /gi=3069303 /ug=Hs.150493 /len=411'	0.210798369	0.010674

Table 5. U95 D Fold Change Genes (>3 over-expressed in Barrett's associated esophageal adenocarcinoma (BA), <0.33 under-expressed in BA)

Affy ID	Gene Name	Fold Change	P-value
78370_at	Cluster Incl. A1053597:q172e03.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1862044 /clone_end=3' /gb=A1053597 /gi=3321384 /ug=Hs.133138 /len=546'	0.209176341	0.001388
82231_at	Cluster Incl. AA367838:EST79039 Homo sapiens cDNA /clone=ATCC-172567 /gb=AA367838 /gi=2020198 /ug=Hs.163834 /len=374	0.208973443	0.000022
73517_at	Cluster Incl. A1865729:wk50e02.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2418842 /clone_end=3' /gb=A1865729 /gi=5529836 /ug=Hs.229800 /len=283'	0.208676712	0.001615
85305_at	Cluster Incl. A1440266:tj01e04.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2140254 /clone_end=3' /gb=A1440266 /gi=4281451 /ug=Hs.170673 /len=461'	0.207370287	0.000035
74891_at	Cluster Incl. AA928646:om75f04.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1553023 /clone_end=3' /gb=AA928646 /gi=3076937 /ug=Hs.234976 /len=488'	0.20599295	0.02766
78399_at	Cluster Incl. A1052543:oz27h04.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1676599 /clone_end=3' /gb=A1052543 /gi=3308534 /ug=Hs.133244 /len=452'	0.204116157	0.001194
77478_at	Cluster Incl. AA977896:qq62b04.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1590895 /clone_end=3' /gb=AA977896 /gi=3155342 /ug=Hs.128873 /len=417'	0.198979696	0.001194
72808_at	Cluster Incl. A1640523:wa29b01.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2299465 /clone_end=3' /gb=A1640523 /gi=4703632 /ug=Hs.223553 /len=442'	0.198366813	0.00004
84903_f_a	Cluster Incl. A1264299:qk20f06.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1869539 /clone_end=3' /gb=A1264299 /gi=3872502 /ug=Hs.166784 /len=396'	0.197923908	0.007339
84077_at	Cluster Incl. A1379425:tc66g04.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2069622 /clone_end=3' /gb=A1379425 /gi=4189278 /ug=Hs.160942 /len=472'	0.195398279	0.002798
85747_at	Cluster Incl. A1610910:tt60a11.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2245148 /clone_end=3' /gb=A1610910 /gi=4620077 /ug=Hs.175357 /len=122'	0.193631412	0.000081
81913_at	Cluster Incl. A1371042:ta29f06.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2045507 /clone_end=3' /gb=A1371042 /gi=4149795 /ug=Hs.160911 /len=484'	0.193436596	0.001955
88656_at	Cluster Incl. A1650477:wa91d08.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2303535 /clone_end=3' /gb=A1650477 /gi=4734456 /ug=Hs.197758 /len=478'	0.190979429	0.037893
69365_at	Cluster Incl. A1703361:wd93d02.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2339139 /clone_end=3' /gb=A1703361 /gi=4991261 /ug=Hs.202354 /len=530'	0.184683765	0.000162

Table 5. U95_D Fold Change Genes (>3 over-expressed in Barrett's associated esophageal adenocarcinoma (BA), <0.33 under-expressed in BA)

Affy ID	Gene Name	Fold Change	P-value
77598_at	Cluster Incl. AA994249:ou05b11.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1625373 /clone_end=3' /gb=AA994249 /gi=3180794 /ug=Hs.129479 /len=414'	0.182835726	0.0023
73971_at	Cluster Incl. AI375662:tc09c10.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2063346 /clone_end=3' /gb=AI375662 /gi=4175652 /ug=Hs.232023 /len=435'	0.181763269	0.001296
82063_at	Cluster Incl. AA552017:ng01g11.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-928196 /clone_end=3' /gb=AA552017 /gi=2322269 /ug=Hs.162245 /len=460'	0.17951496	0.002115
90300_g	Cluster Incl. AA721234:nz72b08.s1 Homo sapiens cDNA /clone=IMAGE-1300983 /gb=AA721234 /gi=2737369 /ug=Hs.121121 /len=345'	0.17343166	0.010479
91925_at	Cluster Incl. AI360231:qy84d11.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2018709 /clone_end=3' /gb=AI360231 /gi=4111852 /ug=Hs.170245 /len=485'	0.171324444	0.029254
79022_at	Cluster Incl. AI821803:nr20b05.x5 Homo sapiens cDNA /clone=IMAGE-1168497 /gb=AI821803 /gi=5440882 /ug=Hs.136580 /len=307'	0.170191727	0.000004
82302_at	Cluster Incl. AI436290:th81c01.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2125056 /clone_end=3' /gb=AI436290 /gi=4309151 /ug=Hs.164162 /len=497'	0.169417008	0.000324
91591_at	Cluster Incl. AI469896:tj88c11.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2148596 /clone_end=3' /gb=AI469896 /gi=4331986 /ug=Hs.158866 /len=459'	0.164920143	0.002275
77589_at	Cluster Incl. AI377752:te56h12.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2090759 /clone_end=3' /gb=AI377752 /gi=4187605 /ug=Hs.129448 /len=429'	0.161975336	0.000178
84438_at	Cluster Incl. AA843562:aj54f01.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1394137 /clone_end=3' /gb=AA843562 /gi=2930080 /ug=Hs.163277 /len=435'	0.15021849	0.003363
74557_s	Cluster Incl. AI739473:wi14a05.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2390192 /clone_end=3' /gb=AI739473 /gi=5101454 /ug=Hs.233630 /len=463'	0.142318725	0.000049
87274_at	Cluster Incl. AA700621:zi43a01.s1 Homo sapiens cDNA, 3 end /clone=433512 /clone_end=3' /gb=AA700621 /gi=2703584 /ug=Hs.188964 /len=519'	0.138942719	0.000066
90647_at	Cluster Incl. AI701529:we36a05.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2343152 /clone_end=3' /gb=AI701529 /gi=4989429 /ug=Hs.129519 /len=507'	0.134163985	0.000207
91481_at	Cluster Incl. AW025687:wu07b01.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2516233 /clone_end=3' /gb=AW025687 /gi=5879217 /ug=Hs.156452 /len=408'	0.132765609	0.000971

Table 5. U95_D Fold Change Genes (>3 over-expressed in Barrett's associated esophageal adenocarcinoma (BA), <0.33 under-expressed in BA)

Affy ID	Gene Name	Fold Change	P-value
89107_s	Cluster Incl. AA1611147:zo74a11.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-592604 /clone_end=3' /gb=AA1611147 /gi=1735384 /ug=Hs.204218 /len=345'	0.131705656	0.048733
77818_at	Cluster Incl. AA927633:om19g09.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1541536 /clone_end=3' /gb=AA927633 /gi=3077054 /ug=Hs.130685 /len=654'	0.129714004	0.000441
87657_at	Cluster Incl. AA699394:zi33d10.s1 Homo sapiens cDNA, 3 end /clone=432595 /clone_end=3' /gb=AA699394 /gi=2702588 /ug=Hs.190348 /len=445'	0.128325924	0.010529
83947_at	Cluster Incl. A1221304:qg74f11.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1840941 /clone_end=3' /gb=A1221304 /gi=3803507 /ug=Hs.160372 /len=410'	0.127051245	0.004949
77148_at	Cluster Incl. AA939266:oa31a09.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1587928 /clone_end=3' /gb=AA939266 /gi=3099179 /ug=Hs.127309 /len=513'	0.126798542	0.01012
81632_i_a	Cluster Incl. A1369347:qy92a02.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2019434 /clone_end=3' /gb=A1369347 /gi=4148100 /ug=Hs.158592 /len=215'	0.126685823	0.000114
91500_at	Cluster Incl. AA069788:zf72h10.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-382531 /clone_end=3' /gb=AA069788 /gi=1577156 /ug=Hs.156880 /len=637'	0.126293774	0.006699
67260_r_a	Cluster Incl. A1383679:tc45h10.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2067619 /clone_end=3' /gb=A1383679 /gi=4196460 /ug=Hs.159114 /len=244'	0.120913902	0.000002
72368_f_a	Cluster Incl. A1583312:ts31g07.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2230236 /clone_end=3' /gb=A1583312 /gi=4569209 /ug=Hs.221671 /len=356'	0.113556615	0.028878
80075_at	Cluster Incl. A1034221:ow09g01.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1646352 /clone_end=3' /gb=A1034221 /gi=3255174 /ug=Hs.146035 /len=432'	0.110154914	0.000049
91129_at	Cluster Incl. A1208356:qg35f06.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1837187 /clone_end=3' /gb=A1208356 /gi=3770298 /ug=Hs.144507 /len=388'	0.106889175	0.0002
69853_at	Cluster Incl. A1798028:wh80e11.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2387084 /clone_end=3' /gb=A1798028 /gi=5363500 /ug=Hs.207474 /len=549'	0.104569948	0.000275
74508_at	Cluster Incl. AW015038:U1-H-B10-aal-a-03-O-U1.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-2709413 /clone_end=3' /gb=AW015038 /gi=5863795 /ug=Hs.233530 /len=423'	0.104558745	0.004341
72462_f_a	Cluster Incl. H40456:yp60d12.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-191831 /clone_end=3' /gb=H40456 /gi=916508 /ug=Hs.221895 /len=418'	0.101016546	0.000992

Table 5. U95_D Fold Change Genes (>3 over-expressed in Barrett's associated esophageal adenocarcinoma (BA), <0.33 under-expressed in BA)

Affy ID	Gene Name	Fold Change	P-value
84947_at	Cluster Incl. AI286188:qi02a08.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1855286 /clone_end=3' /gb=AI286188 /gi=3924421 /ug=Hs.166980 /len=417	0.092519177	0.001823
70855_at	Cluster Incl. AI829652:wf02h07.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2349469 /clone_end=3' /gb=AI829652 /gi=5450323 /ug=Hs.211443 /len=494	0.083077091	0.000164
90484_at	Cluster Incl. AI809578:wf31a09.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2357176 /clone_end=3' /gb=AI809578 /gi=5396144 /ug=Hs.126434 /len=496	0.079933078	0.000211
69162_at	Cluster Incl. AI692566:wd73h03.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2337269 /clone_end=3' /gb=AI692566 /gi=4969906 /ug=Hs.201888 /len=455	0.079613815	0.000067
69526_at	Cluster Incl. AA158249:zo76c07.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-592812 /clone_end=3' /gb=AA158249 /gi=1733044 /ug=Hs.203537 /len=580	0.075582558	0.000006
91579_at	Cluster Incl. AI939511:qy28e02.x5 Homo sapiens cDNA, 3 end /clone=IMAGE-2013338 /clone_end=3' /gb=AI939511 /gi=5678300 /ug=Hs.158678 /len=547	0.06757725	0.00086
86283_r_a	Cluster Incl. T47055:yb12g05.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-71000 /clone_end=3' /gb=T47055 /gi=649038 /ug=Hs.182019 /len=348	0.067022858	0.005615
84082_at	Cluster Incl. AI566771:tg67e02.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2213882 /clone_end=3' /gb=AI566771 /gi=4525223 /ug=Hs.160953 /len=461	0.059933336	0.00077
83466_at	Cluster Incl. AA468767:ne09e12.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-880750 /clone_end=3' /gb=AA468767 /gi=2195301 /ug=Hs.178337 /len=442	0.057826652	0
73402_at	Cluster Incl. AA781220:ai48a03.s1 Homo sapiens cDNA, 3 end /clone=1360012 /clone_end=3' /gb=AA781220 /gi=2840551 /ug=Hs.226722 /len=426	0.052624187	0.000058
84869_at	Cluster Incl. AI123917:qa37e01.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1688952 /clone_end=3' /gb=AI123917 /gi=3539683 /ug=Hs.166597 /len=495	0.049170602	0.000018
73243_at	Cluster Incl. AI199897:qf84a05.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1756688 /clone_end=3' /gb=AI199897 /gi=3752503 /ug=Hs.225137 /len=563	0.045513684	0
73485_at	Cluster Incl. T71258:yd35b05.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-110193 /clone_end=3' /gb=T71258 /gi=685779 /ug=Hs.228790 /len=517	0.041793009	0.000017
75857_at	Cluster Incl. W80832:zd90g02.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-356786 /clone_end=3' /gb=W80832 /gi=1391875 /ug=Hs.116773 /len=467	0.035564271	0.000051

Table 5. U95_D Fold Change Genes (>3 over-expressed in Barrett's associated esophageal adenocarcinoma (BA), <0.33 under-expressed in BA)

Affy ID	Gene Name	Fold Change	P-value
90122_f_a	Cluster Incl. AW025309:wu73c09.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-990947 /clone_end=3' /gb=AW025309 /gj=5878839 /ug=Hs.113165 /len=497'	0.024715815	0
91361_at	Cluster Incl. AI265958:qq90h05.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1938681 /clone_end=3' /gb=AI265958 /gj=3884116 /ug=Hs.150821 /len=490'	0.017169688	0.00001
84270_at	Cluster Incl. AI829641:wf02g08.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2349470 /clone_end=3' /gb=AI829641 /gj=5450312 /ug=Hs.162204 /len=348'	0.014034927	0.003989
69149_at	Cluster Incl. AI282714:qt65b06.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1960115 /clone_end=3' /gb=AI282714 /gj=3920947 /ug=Hs.201877 /len=412'	0.012878608	0.00022

Table 6. U95_E Fold Change Genes (>3 over-expressed in Barrett's associated esophageal adenocarcinoma (BA), <0.33 under-expressed in BA)

Affy ID	Gene Name	Fold Change	P-value
88567_s	Cluster Incl. AI344053:tc01h08.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2062623 /clone_end=3' /gb=AI344053 /gi=4081259 /ug=Hs.115838 /len=449'	33.12163404	0.000003
76739_at	Cluster Incl. AI337014:qx87g02.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2009522 /clone_end=3' /gb=AI337014 /gi=4073941 /ug=Hs.132989 /len=679'	24.46364831	0
83365_at	Cluster Incl. AI341602:qx92g05.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2010008 /clone_end=3' /gb=AI341602 /gi=4078529 /ug=Hs.152932 /len=461'	21.6308226	0.001328
81562_at	Cluster Incl. AI733811:qk04h06.x5 Homo sapiens cDNA, 3 end /clone=IMAGE-1868027 /clone_end=3' /gb=AI733811 /gi=5054924 /ug=Hs.121194 /len=609'	20.13979542	0.000018
73111_s	Cluster Incl. AI859854:wm21c10.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2436594 /clone_end=3' /gb=AI859854 /gi=5513459 /ug=Hs.234479 /len=455'	19.38056138	0.000001
90421_at	Cluster Incl. AA633203:nq57b02.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1147947 /clone_end=3' /gb=AA633203 /gi=2556617 /ug=Hs.14258 /len=570'	19.2499917	0.000051
88580_at	Cluster Incl. AI275140:ql70h02.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1877715 /clone_end=3' /gb=AI275140 /gi=3897414 /ug=Hs.116104 /len=444'	18.08284727	0.000109
78328_at	Cluster Incl. AI691066:wf22b05.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2351313 /clone_end=3' /gb=AI691066 /gi=4902368 /ug=Hs.165619 /len=448'	15.78241233	0.000067
89808_at	Cluster Incl. AA628967:af28h06.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1033019 /clone_end=3' /gb=AA628967 /gi=2541354 /ug=Hs.115274 /len=753'	15.29942334	0.00001
90582_at	Cluster Incl. AI688604:wc90f10.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2325931 /clone_end=3' /gb=AI688604 /gi=4899898 /ug=Hs.154903 /len=454'	15.09542862	0.000754
87884_at	Cluster Incl. AI922828:wo14e03.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2455324 /clone_end=3' /gb=AI922828 /gi=5658792 /ug=Hs.236102 /len=548'	14.54781052	0.00033
68693_at	Cluster Incl. T69015:yc31f04.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-82303 /clone_end=3' /gb=T69015 /gi=680163 /ug=Hs.192728 /len=478'	14.08619278	0.000013
73054_at	Cluster Incl. C06075:C06075 Homo sapiens cDNA /clone=hbc5496 /gb=C06075 /gi=1502851 /ug=Hs.234147 /len=454	11.3375198	0.012822

Table 6. U95_E Fold Change Genes (>3 over-expressed in Barrett's associated esophageal adenocarcinoma (BA), <0.33 under-expressed in BA)

Affy ID	Gene Name	Fold Change	P-value
81774_at	Cluster Incl. A1683036:tw48f06.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2262947 /clone_end=3' /gb=A1683036 /gi=4893218 /ug=Hs.124135 /len=482'	10.36686915	0.004902
82840_at	Cluster Incl. A1799626:to74b03.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2183981 /clone_end=3' /gb=A1799626 /gi=5365098 /ug=Hs.145807 /len=558'	10.18825096	0.000015
88504_at	Cluster Incl. A1955239:wx31f07.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2545285 /clone_end=3' /gb=A1955239 /gi=5747549 /ug=Hs.112460 /len=467'	9.83796577	0.002999
77510_at	Cluster Incl. AA088446:z189f04.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-511807 /clone_end=3' /gb=AA088446 /gi=1633958 /ug=Hs.170298 /len=590'	9.77410756	0.000003
78379_at	Cluster Incl. A1684746:wa85f10.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2302987 /clone_end=3' /gb=A1684746 /gi=4896040 /ug=Hs.119274 /len=768'	9.652586214	0.000012
73464_r_a	Cluster Incl. AA648038:HGBBT038 Homo sapiens cDNA /gb=AA648038 /gi=2574467 /ug=Hs.95614 /len=180	9.485196734	0.002348
90136_at	Cluster Incl. A1638295:tt09b11.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2240253 /clone_end=3' /gb=A1638295 /gi=4690529 /ug=Hs.128685 /len=547'	9.024823944	0.001058
73826_at	Cluster Incl. A1971242:wr27a01.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2488872 /clone_end=3' /gb=A1971242 /gi=5768068 /ug=Hs.124854 /len=453'	8.515076242	0.000011
84271_r_a	Cluster Incl. AW025560:wu97h02.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-990982 /clone_end=3' /gb=AW025560 /gi=5879090 /ug=Hs.166398 /len=458'	7.818636431	0.002861
73493_at	Cluster Incl. AA701983:z170a04.s1 Homo sapiens cDNA, 3 end /clone=436110 /clone_end=3' /gb=AA701983 /gi=2705096 /ug=Hs.114085 /len=522'	7.302601124	0.00004
76364_at	Cluster Incl. AA643507:nq86f06.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1159235 /clone_end=3' /gb=AA643507 /gi=2568725 /ug=Hs.124840 /len=509'	6.913074606	0.001015
91095_s	Cluster Incl. AA535819:nj79e01.s1 Homo sapiens cDNA /clone=IMAGE-998712 /gb=AA535819 /gi=2280072 /ug=Hs.238355 /len=522	6.873901823	0.002754
81623_at	Cluster Incl. A1208954:qg29e05.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1836608 /clone_end=3' /gb=A1208954 /gi=3770896 /ug=Hs.121876 /len=418'	6.825834554	0.001662
81690_at	Cluster Incl. A1093231:qb04b09.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1695257 /clone_end=3' /gb=A1093231 /gi=3432207 /ug=Hs.122910 /len=451'	6.794338221	0.000834

Table 6. U95_E Fold Change Genes (>3 over-expressed in Barrett's associated esophageal adenocarcinoma (BA), <0.33 under-expressed in BA)

Affy ID	Gene Name	Fold Change	P-value
81932_at	Cluster Incl. AI659966:we64e02.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2345882 /clone_end=3' /gb=AI659966 /gi=4763536 /ug=Hs.126478 /len=490'	6.724516081	0.00524
77540_at	Cluster Incl. AA007367:zh98b03.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-429293 /clone_end=3' /gb=AA007367 /gi=1463371 /ug=Hs.173088 /len=462'	6.57607309	0.003018
73238_at	Cluster Incl. AI457905:ij48b10.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2144731 /clone_end=3' /gb=AI457905 /gi=4310796 /ug=Hs.235943 /len=546'	6.48771467	0.006137
85141_at	Cluster Incl. AI192838:qe63c04.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1743654 /clone_end=3' /gb=AI192838 /gi=3744047 /ug=Hs.183053 /len=444'	6.18069379	0.002186
85126_at	Cluster Incl. AI751438:cn10a03.y1 Homo sapiens cDNA /clone=NHTBC_cn10a03-(random) /gb=AI751438 /gi=5129702 /ug=Hs.182827 /len=513'	6.087887372	0.00056
81668_at	Cluster Incl. AI346446:qp45a07.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1925940 /clone_end=3' /gb=AI346446 /gi=4083652 /ug=Hs.122587 /len=470'	6.04859158	0.000438
88155_at	Cluster Incl. AI125923:qc41f07.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1712197 /clone_end=3' /gb=AI125923 /gi=3594437 /ug=Hs.239324 /len=512'	5.967007568	0.020546
88222_at	Cluster Incl. AW013949:U1-H-B10-aad-g-11-0-U1.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-2708949 /clone_end=3' /gb=AW013949 /gi=5862706 /ug=Hs.239673 /len=361'	5.934357544	0.000747
80604_at	Cluster Incl. AW007566:wf02e03.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2506300 /clone_end=3' /gb=AW007566 /gi=5856429 /ug=Hs.239193 /len=624'	5.811542288	0.015477
67197_r_a	Cluster Incl. AI187329:qe26c02.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1740098 /clone_end=3' /gb=AI187329 /gi=3737967 /ug=Hs.182051 /len=483'	5.794363406	0.031677
77572_at	Cluster Incl. AI740961:wg18g09.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2365504 /clone_end=3' /gb=AI740961 /gi=5109249 /ug=Hs.179791 /len=538'	5.69131656	0.000179
88041_at	Cluster Incl. AI984261:wz57h06.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2562203 /clone_end=3' /gb=AI984261 /gi=5811480 /ug=Hs.238551 /len=486'	5.620260813	0.000122
85197_at	Cluster Incl. H53229:yq84e08.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-202502 /clone_end=5' /gb=H53229 /gi=993376 /ug=Hs.183775 /len=529'	5.587699119	0.001786
90566_at	Cluster Incl. AI831961:wh90b03.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2387981 /clone_end=3' /gb=AI831961 /gi=5452632 /ug=Hs.153850 /len=496'	5.56730113	0.023455

Table 6. U95_E Fold Change Genes (>3 over-expressed in Barrett's associated esophageal adenocarcinoma (BA), <0.33 under-expressed in BA)

Affy ID	Gene Name	Fold Change	P-value
84480_at	Cluster Incl. A1821052:nr06c07.y5 Homo sapiens cDNA, 5 end /clone=IMAGE-1161036 /clone_end=5' /gb=A1821052 /gi=5440131 /ug=Hs.168974 /len=579'	5.510588082	0.003876
87888_s	Cluster Incl. A1611162:tw39g10.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2262114 /clone_end=3' /gb=A1611162 /gi=4620329 /ug=Hs.236173 /len=513'	5.340707416	0.001304
91873_s	Cluster Incl. A1690773:tx99c07.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2277708 /clone_end=3' /gb=A1690773 /gi=4902075 /ug=Hs.133294 /len=368'	5.339491382	0.016636
73036_r_a	Cluster Incl. AA602984:np31e11.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1117964 /clone_end=3' /gb=AA602984 /gi=2436845 /ug=Hs.234035 /len=487'	5.273912907	0.0033
76463_at	Cluster Incl. AW007116:wt09d07.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2506957 /clone_end=3' /gb=AW007116 /gi=5855894 /ug=Hs.127007 /len=521'	5.263622629	0.000009
82385_at	Cluster Incl. AA534591:nf81b04.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-926287 /clone_end=3' /gb=AA534591 /gi=2278844 /ug=Hs.135657 /len=492'	5.252002344	0.011367
82482_r_a	Cluster Incl. H07125:yl82e05.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-44497 /clone_end=3' /gb=H07125 /gi=870657 /ug=Hs.138418 /len=526'	5.144291508	0.005336
69197_r_a	Cluster Incl. AA508552:nh67b08.s1 Homo sapiens cDNA /clone=IMAGE-957399 /gb=AA508552 /gi=2246055 /ug=Hs.195839 /len=315	5.137532156	0.001736
67549_at	Cluster Incl. AA001232:zh82g06.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-427834 /clone_end=5' /gb=AA001232 /gi=1437355 /ug=Hs.186593 /len=473'	5.065760716	0.00041
70873_at	Cluster Incl. A1807627:wf49b09.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2358905 /clone_end=3' /gb=A1807627 /gi=5394193 /ug=Hs.209978 /len=530'	5.04405858	0.000025
73800_at	Cluster Incl. A1890347:wm84b05.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2442609 /clone_end=3' /gb=A1890347 /gi=5595511 /ug=Hs.124380 /len=620'	4.884088199	0.000153
70170_f_a	Cluster Incl. A1251913:qu76a04.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1977966 /clone_end=3' /gb=A1251913 /gi=3848442 /ug=Hs.203582 /len=289'	4.811398521	0.002454
69170_at	Cluster Incl. A1990825:ws32c05.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2498888 /clone_end=3' /gb=A1990825 /gi=5837706 /ug=Hs.195398 /len=549'	4.779712151	0.033749
74042_g	Cluster Incl. A1732208:ne53h01.x5 Homo sapiens cDNA, 3 end /clone=IMAGE-901105 /clone_end=3' /gb=A1732208 /gi=5053321 /ug=Hs.126783 /len=536'	4.765311344	0.006798

Table 6. U95_E Fold Change Genes (>3 over-expressed in Barrett's associated esophageal adenocarcinoma (BA), <0.33 under-expressed in BA)

Affy ID	Gene Name	Fold Change	P-value
88923_at	Cluster Incl. AW025183:wu72c05.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-990843 /clone_end=3' /gb=AW025183 /gi=5878713 /ug=Hs.127680 /len=504'	4.616589303	0.000839
89983_at	Cluster Incl. A1762857:wi63b04.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2397967 /clone_end=3' /gb=A1762857 /gi=5178524 /ug=Hs.123177 /len=554'	4.571238045	0.004145
88043_g	Cluster Incl. A1984261:wz57h06.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2562203 /clone_end=3' /gb=A1984261 /gi=5811480 /ug=Hs.238551 /len=486'	4.56014179	0.001077
82985_at	Cluster Incl. A1817781:wk40b08.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2417847 /clone_end=3' /gb=A1817781 /gi=5436860 /ug=Hs.146905 /len=470'	4.501873026	0.038048
67667_at	Cluster Incl. R02826:ye80g11.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-124100 /clone_end=3' /gb=R02826 /gi=752562 /ug=Hs.187456 /len=371'	4.458109865	0.008755
74965_at	Cluster Incl. A1075710:oz24f10.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1676299 /clone_end=3' /gb=A1075710 /gi=3404888 /ug=Hs.133988 /len=458'	4.433933192	0.000294
81447_at	Cluster Incl. A1540087:td09b08.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2075127 /clone_end=3' /gb=A1540087 /gi=4457460 /ug=Hs.120243 /len=489'	4.336850383	0.034037
85757_at	Cluster Incl. A1635504:ts95a01.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2238984 /clone_end=3' /gb=A1635504 /gi=4686834 /ug=Hs.191229 /len=496'	4.307200411	0.001228
86946_s	Cluster Incl. AL044106:DKFZp434M0528 s1 Homo sapiens cDNA, 3 end /clone=DKFZp434M0528 /clone_end=3' /gb=AL044106 /gi=5432332 /ug=Hs.209359 /len=574'	4.274201098	0.000009
78442_at	Cluster Incl. A1819340:wg61a01.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2369544 /clone_end=3' /gb=A1819340 /gi=5438419 /ug=Hs.13561 /len=539'	4.255225315	0.03273
77354_at	Cluster Incl. A1935827:wo51c06.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2458858 /clone_end=3' /gb=A1935827 /gi=5674697 /ug=Hs.161791 /len=533'	4.221724462	0.000009
73264_f_a	Cluster Incl. AW025939:wu09c06.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2516458 /clone_end=3' /gb=AW025939 /gi=5879469 /ug=Hs.236356 /len=326'	4.184011102	0.012722
82129_at	Cluster Incl. A1914323:wd77d01.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2337601 /clone_end=3' /gb=A1914323 /gi=5634178 /ug=Hs.131175 /len=543'	4.163620114	0.007416
77848_f_a	Cluster Incl. AA018663:ze53f11.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-362733 /clone_end=3' /gb=AA018663 /gi=1481928 /ug=Hs.204007 /len=496'	4.141843067	0.001411

Table 6. U95_E Fold Change Genes (>3 over-expressed in Barrett's associated esophageal adenocarcinoma (BA), <0.33 under-expressed in BA)

Affy ID	Gene Name	Fold Change	P-value
82858_at	Cluster Incl. A1754693:cr28h02.x1 Homo sapiens cDNA, 3 end /clone=HBMSC_cr28h02 /clone_end=3' /gb=A1754693 /gi=5132957 /ug=Hs.145968 /len=515'	4.138901583	0.000443
87558_f_a	Cluster Incl. W85857:zh52f11.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-415725 /clone_end=3' /gb=W85857 /gi=1398355 /ug=Hs.226604 /len=446'	4.078971064	0.015864
76571_at	Cluster Incl. A1820585:os03a03.x5 Homo sapiens cDNA, 3 end /clone=IMAGE-1604236 /clone_end=3' /gb=A1820585 /gi=5439664 /ug=Hs.129107 /len=538'	4.07737079	0.00185
AFFX-Bio	J04423 E coli bioB gene biotin synthetase (-5, -M, -3 represent transcript regions 5 prime, Middle, and 3 prime respectively)	4.074822599	0.006154
77364_at	Cluster Incl. A1676059:wc04g08.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2314238 /clone_end=3' /gb=A1676059 /gi=4876539 /ug=Hs.163900 /len=562'	4.032646341	0.027423
79405_at	Cluster Incl. AA740146:ob26a07.s1 Homo sapiens cDNA /clone=IMAGE-1324788 /gb=AA740146 /gi=2778738 /ug=Hs.192397 /len=460	4.01839873	0.013599
90224_at	Cluster Incl. A1276259:ql65f03.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1877213 /clone_end=3' /gb=A1276259 /gi=3898533 /ug=Hs.13337 /len=505'	4.004273997	0.008055
87802_at	Cluster Incl. AA613291:nc39d04.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1103047 /clone_end=3' /gb=AA613291 /gi=2464329 /ug=Hs.234346 /len=482'	3.985917634	0.004647
87684_at	Cluster Incl. AW007058:ws49f05.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2500545 /clone_end=3' /gb=AW007058 /gi=5855836 /ug=Hs.232261 /len=345'	3.965226206	0.017504
82496_at	Cluster Incl. AA832417:oc99d03.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1357829 /clone_end=3' /gb=AA832417 /gi=2905516 /ug=Hs.139650 /len=402'	3.933719194	0.022181
89253_at	Cluster Incl. A1653050:wb42h02.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2308371 /clone_end=3' /gb=A1653050 /gi=4737029 /ug=Hs.162717 /len=698'	3.928266882	0.000754
78846_at	Cluster Incl. AA931876:oc58f04.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1570399 /clone_end=3' /gb=AA931876 /gi=3086262 /ug=Hs.181245 /len=489'	3.910353677	0.005377
88840_at	Cluster Incl. A1393205:tg14b07.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2108725 /clone_end=3' /gb=A1393205 /gi=4222752 /ug=Hs.126265 /len=614'	3.900166459	0.01782
86478_at	Cluster Incl. A1741566:wg21g12.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2365798 /clone_end=3' /gb=A1741566 /gi=5109854 /ug=Hs.200099 /len=614'	3.89585652	0.000249

Table 6. U95_E Fold Change Genes (>3 over-expressed in Barrett's associated esophageal adenocarcinoma (BA), <0.33 under-expressed in BA)

Affy ID	Gene Name	Fold Change	P-value
89973_at	Cluster Incl. A1656161:tt43g10.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2243586 /clone_end=3' /gb=A1656161 /gi=4740140 /ug=Hs.122810 /len=542'	3.853888055	0.003549
69247_at	Cluster Incl. A1984074:wz56c02.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2562050 /clone_end=3' /gb=A1984074 /gi=5811293 /ug=Hs.196398 /len=614'	3.846943175	0.002703
77225_at	Cluster Incl. A1740516:wg16a11.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2365244 /clone_end=3' /gb=A1740516 /gi=5108804 /ug=Hs.152812 /len=591'	3.845535109	0.003211
90524_at	Cluster Incl. A1889361:wm98b08.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2443959 /clone_end=3' /gb=A1889361 /gi=5594525 /ug=Hs.148289 /len=486'	3.806709116	0.032956
72388_at	Cluster Incl. AA608808:af04e10.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1030698 /clone_end=3' /gb=AA608808 /gi=2457236 /ug=Hs.225118 /len=393'	3.793457244	0.000011
84407_r_a	Cluster Incl. A1032906:ox19e08.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1656806 /clone_end=3' /gb=A1032906 /gi=3253859 /ug=Hs.167800 /len=471'	3.767444971	0.00167
75621_at	Cluster Incl. A1935035:wd17g08.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2328446 /clone_end=3' /gb=A1935035 /gi=5673905 /ug=Hs.145656 /len=483'	3.764029378	0.048154
82539_at	Cluster Incl. A1935586:wo98c05.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2463368 /clone_end=3' /gb=A1935586 /gi=5674456 /ug=Hs.142869 /len=516'	3.761588053	0.004131
90265_at	Cluster Incl. AW050627:wz19e03.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2558524 /clone_end=3' /gb=AW050627 /gi=5912897 /ug=Hs.135183 /len=477'	3.751652632	0.000052
81787_i_a	Cluster Incl. A1425019:tg50c11.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2112212 /clone_end=3' /gb=A1425019 /gi=4270950 /ug=Hs.124280 /len=509'	3.729431315	0.020585
81953_at	Cluster Incl. A1733253:oo60c07.x5 Homo sapiens cDNA, 3 end /clone=IMAGE-1570572 /clone_end=3' /gb=A1733253 /gi=5054366 /ug=Hs.126860 /len=531'	3.673677735	0.001218
89731_at	Cluster Incl. A1017165:ou28a11.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1627580 /clone_end=3' /gb=A1017165 /gi=3231501 /ug=Hs.104573 /len=461'	3.660093991	0.026076
88214_at	Cluster Incl. A1473909:tf68d07.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2137165 /clone_end=3' /gb=A1473909 /gi=4326954 /ug=Hs.239658 /len=402'	3.657078333	0.001554
71534_at	Cluster Incl. AA584378:nm77b04.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1089871 /clone_end=3' /gb=AA584378 /gi=2368987 /ug=Hs.219473 /len=404'	3.64418462	0.000698

Table 6. U95_E Fold Change Genes (>3 over-expressed in Barrett's associated esophageal adenocarcinoma (BA), <0.33 under-expressed in BA)

Affy ID	Gene Name	Fold Change	P-value
91313_at	Cluster Incl. AA131041:zo16e03.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-587068 /clone_end=3' /gb=AA131041 /gi=1692593 /ug=Hs.82554 /len=539'	3.641675284	0.003603
74698_at	Cluster Incl. AW003102:wr03e03.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2480476 /clone_end=3' /gb=AW003102 /gi=5849940 /ug=Hs.131886 /len=512'	3.636444818	0.004914
76293_at	Cluster Incl. AI632750:wa33g09.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2299936 /clone_end=3' /gb=AI632750 /gi=4684080 /ug=Hs.121233 /len=519'	3.614166118	0.001198
67246_at	Cluster Incl. AI040381:ox16c09.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1656496 /clone_end=3' /gb=AI040381 /gi=3279575 /ug=Hs.182430 /len=535'	3.607391355	0.010336
76041_g	Cluster Incl. AI492574:ti29f08.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2131911 /clone_end=3' /gb=AI492574 /gi=4393577 /ug=Hs.234190 /len=535'	3.554944957	0.001981
91762_at	Cluster Incl. AA496243:zx70g12.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-796870 /clone_end=3' /gb=AA496243 /gi=2229564 /ug=Hs.84640 /len=579'	3.524153823	0.004236
76137_at	Cluster Incl. AA639753:nq82c12.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1158838 /clone_end=3' /gb=AA639753 /gi=2563532 /ug=Hs.116462 /len=645'	3.523452759	0.005364
87456_at	Cluster Incl. AI990471:ws40a05.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2499632 /clone_end=3' /gb=AI990471 /gi=5837352 /ug=Hs.224630 /len=497'	3.511142884	0.000815
80760_i_a	Cluster Incl. AI888428:wn20h08.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2446047 /clone_end=3' /gb=AI888428 /gi=5593515 /ug=Hs.5402 /len=395'	3.509284285	0.024008
88678_at	Cluster Incl. AF121164:AF121164 Homo sapiens cDNA /clone=PFGTG1-2 /gb=AF121164 /gi=4886240 /ug=Hs.120879 /len=654	3.494772543	0.001841
90509_at	Cluster Incl. AI968197:wu14c07.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2516940 /clone_end=3' /gb=AI968197 /gi=5765015 /ug=Hs.14587 /len=541'	3.477306776	0.010461
73188_s	Cluster Incl. AA948682:qq49b11.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1589661 /clone_end=3' /gb=AA948682 /gi=3109935 /ug=Hs.235393 /len=411'	3.462332464	0.003352
74964_at	Cluster Incl. AA045735:zk81g12.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-489286 /clone_end=3' /gb=AA045735 /gi=1525629 /ug=Hs.133961 /len=399'	3.461482296	0.000176
89166_at	Cluster Incl. AI953998:wx78c12.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2549782 /clone_end=3' /gb=AI953998 /gi=5746308 /ug=Hs.152510 /len=679'	3.455539647	0.000616

Table 6. U95_E Fold Change Genes (>3 over-expressed in Barrett's associated esophageal adenocarcinoma (BA), <0.33 under-expressed in BA)

Affy ID	Gene Name	Fold Change	P-value
90732_at	Cluster Incl. W45137:zc81g05.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-328760 /clone_end=3' /gb=W45137 /gi=1329442 /ug=Hs.183576 /len=481'	3.437671708	0.001008
69037_r_a	Cluster Incl. AA730798:nw49b12.s1 Homo sapiens cDNA /clone=IMAGE-1249919 /gb=AA730798 /gi=2752002 /ug=Hs.194135 /len=310	3.434365508	0.02404
84983_at	Cluster Incl. A1741880:wg48b12.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2368319 /clone_end=3' /gb=A1741880 /gi=5110255 /ug=Hs.179891 /len=454'	3.429078419	0.022269
92067_s	Cluster Incl. A1348900:ta98e05.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2052128 /clone_end=3' /gb=A1348900 /gi=4086106 /ug=Hs.25199 /len=420'	3.420352947	0.031666
80859_at	Cluster Incl. A1684877:wa86f08.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2303079 /clone_end=3' /gb=A1684877 /gi=4896171 /ug=Hs.105489 /len=768'	3.414213425	0.000763
75954_at	Cluster Incl. A1978606:wr57b07.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2491765 /clone_end=3' /gb=A1978606 /gi=5803636 /ug=Hs.201615 /len=585'	3.410569117	0.019697
74159_at	Cluster Incl. AA534390:nf79h07.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-926173 /clone_end=3' /gb=AA534390 /gi=2278643 /ug=Hs.127762 /len=588'	3.401564012	0.029962
76075_at	Cluster Incl. AW014657:U1-H-B10p-aaw-b-11-O-U1.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-2710628 /clone_end=3' /gb=AW014557 /gi=5863314 /ug=Hs.112420 /len=618'	3.375380748	0.006718
90203_at	Cluster Incl. A1819204:wj32f08.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2404551 /clone_end=3' /gb=A1819204 /gi=5438283 /ug=Hs.132743 /len=514'	3.345450186	0.000782
89795_at	Cluster Incl. AL040892:DKFZp434l1715_s1 Homo sapiens cDNA, 3 end /clone=DKFZp434l1715 /clone_end=3' /gb=AL040892 /gi=5409837 /ug=Hs.114173 /len=717'	3.343086565	0.01438
86866_r_a	Cluster Incl. A1765629:wi82e01.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2399832 /clone_end=3' /gb=A1765629 /gi=5232138 /ug=Hs.207278 /len=332'	3.315297451	0.010622
87205_at	Cluster Incl. AA419233:zv35f05.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-755649 /clone_end=3' /gb=AA419233 /gi=2078997 /ug=Hs.215682 /len=423'	3.312326275	0.004096
78393_at	Cluster Incl. AA725820:ai25b05.s1 Homo sapiens cDNA, 3 end /clone=1343793 /clone_end=3' /gb=AA725820 /gi=2743527 /ug=Hs.123426 /len=472'	3.311882393	0.021412
74179_at	Cluster Incl. A1889959:wm65f08.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2440839 /clone_end=3' /gb=A1889959 /gi=5595123 /ug=Hs.127797 /len=479'	3.305411403	0.004734

Table 6. U95_E Fold Change Genes (>3 over-expressed in Barrett's associated esophageal adenocarcinoma (BA), <0.33 under-expressed in BA)

Affy ID	Gene Name	Fold Change	P-value
89306_at	Cluster Incl. AI934965:wd17a03.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2328364 /clone_end=3' /gb=AI934965 /gi=5673835 /ug=Hs.181261 /len=588'	3.300123522	0.020207
69031_at	Cluster Incl. AI686521:tu34g02.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2252978 /clone_end=3' /gb=AI686521 /gi=4897815 /ug=Hs.194118 /len=597'	3.296015126	0.011834
88302_at	Cluster Incl. AI082708:ox59f01.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1660633 /clone_end=3' /gb=AI082708 /gi=3419500 /ug=Hs.31588 /len=369'	3.287284047	0.009528
78861_f_a	Cluster Incl. H18887:yn52d11.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-172053 /clone_end=3' /gb=H18887 /gi=885127 /ug=Hs.181836 /len=401'	3.283264496	0.000041
81733_at	Cluster Incl. AI632972:bx55h08.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2273535 /clone_end=3' /gb=AI632972 /gi=4684302 /ug=Hs.123370 /len=562'	3.270101441	0.001223
90603_at	Cluster Incl. AI916544:wa26h03.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2299253 /clone_end=3' /gb=AI916544 /gi=5636399 /ug=Hs.158549 /len=475'	3.268418769	0.013059
71228_at	Cluster Incl. AI919493:tp22a03.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2188492 /clone_end=3' /gb=AI919493 /gi=5639348 /ug=Hs.212925 /len=320'	3.264815022	0.016554
69060_at	Cluster Incl. AI681180:bx44h02.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2272467 /clone_end=3' /gb=AI681180 /gi=4891362 /ug=Hs.189394 /len=489'	3.258903714	0.003186
81731_at	Cluster Incl. AA811371:ob82b10.s1 Homo sapiens cDNA /clone=IMAGE-1337851 /gb=AA811371 /gi=2880982 /ug=Hs.123362 /len=482'	3.254465131	0.008956
80538_s	Cluster Incl. AW020375:df08h01.y1 Homo sapiens cDNA, 5 end /clone=IMAGE-2483185 /clone_end=5' /gb=AW020375 /gi=5873905 /ug=Hs.238653 /len=339'	3.238426465	0.000033
83130_at	Cluster Incl. AI683864:tw54a08.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2263478 /clone_end=3' /gb=AI683864 /gi=4894046 /ug=Hs.149264 /len=489'	3.237963905	0.002982
86750_at	Cluster Incl. AI888991:wj16b04.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2402959 /clone_end=3' /gb=AI888991 /gi=5594155 /ug=Hs.204044 /len=528'	3.22255218	0.002743
82094_i_a	Cluster Incl. AI810266:wb86h07.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2312605 /clone_end=3' /gb=AI810266 /gi=5396832 /ug=Hs.130853 /len=553'	3.218521352	0.031896
80080_at	Cluster Incl. AI916889:wb46g08.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2308766 /clone_end=3' /gb=AI916889 /gi=5636744 /ug=Hs.213436 /len=480'	3.213809716	0.003436

Table 6. U95_E Fold Change Genes (>3 over-expressed in Barrett's associated esophageal adenocarcinoma (BA), <0.33 under-expressed in BA)

Affy ID	Gene Name	Fold Change	P-value
76779_at	Cluster Incl. AW014285:U1-H-B10-aak-h-03-0-U1.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-2709748 /clone_end=3' /gb=AW014285 /gi=5863042 /ug=Hs.133925 /len=493'	3.210119895	0.012957
88103_s_	Cluster Incl. AW007018:ws49b'0.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2500507 /clone_end=3' /gb=AW007018 /gi=5855796 /ug=Hs.239125 /len=524'	3.190608857	0.030944
88452_at	Cluster Incl. A1625821:ty65b01.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2283913 /clone_end=3' /gb=A1625821 /gi=4650752 /ug=Hs.101320 /len=647'	3.188760476	0.004402
78788_at	Cluster Incl. A1674088:wd18a08.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2328470 /clone_end=3' /gb=A1674088 /gi=4874568 /ug=Hs.8122 /len=576'	3.185705139	0.013029
75722_at	Cluster Incl. AA766775:oa35d08.s1 Homo sapiens cDNA /clone=IMAGE-1306959 /gb=AA766775 /gi=2818013 /ug=Hs.163195 /len=440'	3.176732451	0.004027
85325_at	Cluster Incl. W89075:zh73a10.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-417690 /clone_end=3' /gb=W89075 /gi=1404168 /ug=Hs.186182 /len=456'	3.174084701	0.001733
72349_at	Cluster Incl. D29047:HUMNK041 Homo sapiens cDNA /clone=041 /gb=D29047 /gi=598980 /ug=Hs.224812 /len=418'	3.169517307	0.000389
85939_at	Cluster Incl. A1694139:wd89c05.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2338760 /clone_end=3' /gb=A1694139 /gi=4971479 /ug=Hs.192855 /len=330'	3.161612049	0.02562
79188_r_a	Cluster Incl. T72642:yd19d02.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-108675 /clone_end=3' /gb=T72642 /gi=689317 /ug=Hs.191118 /len=428'	3.154189137	0.009489
87790_at	Cluster Incl. AW015585:U1-H-B10p-aau-h-09-0-U1.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-2710888 /clone_end=3' /gb=AW015585 /gi=5864342 /ug=Hs.234252 /len=630'	3.153789914	0.000844
89603_at	Cluster Incl. R77227:y72c10.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-144786 /clone_end=3' /gb=R77227 /gi=851859 /ug=Hs.237156 /len=449'	3.137562053	0.004856
84981_r_a	Cluster Incl. T54146:ya92h02.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-69171 /clone_end=3' /gb=T54146 /gi=656007 /ug=Hs.179847 /len=559'	3.123046617	0.031758
81355_at	Cluster Incl. AA946617:ox38e04.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1588638 /clone_end=3' /gb=AA946617 /gi=3110012 /ug=Hs.119183 /len=525'	3.109445352	0.008631
87837_at	Cluster Incl. A1656113:tt38c07.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2243052 /clone_end=3' /gb=A1656113 /gi=4740092 /ug=Hs.235408 /len=436'	3.097465077	0.0051

Table 6. U95_E Fold Change Genes (>3 over-expressed in Barrett's associated esophageal adenocarcinoma (BA), <0.33 under-expressed in BA)

Affy ID	Gene Name	Fold Change	P-value
91875_s	Cluster Incl. AI053741.qi69h07.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1861789 /clone_end=3' /gb=AI053741 /gi=3321528 /ug=Hs.133294 /len=337	3.095993734	0.017489
83569_at	Cluster Incl. AI823960.wj21d05.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2403465 /clone_end=3' /gb=AI823960 /gi=5444631 /ug=Hs.155718 /len=420	3.088550292	0.044324
83331_at	Cluster Incl. AA568924.nm23b06.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1060979 /clone_end=3' /gb=AA568924 /gi=2341978 /ug=Hs.152484 /len=475	3.075127644	0.007888
84009_at	Cluster Incl. AA218643.zq14c10.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-629682 /clone_end=3' /gb=AA218643 /gi=1832735 /ug=Hs.161690 /len=460	3.073579917	0.000394
86916_at	Cluster Incl. R24723.yg43c04.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-35336 /clone_end=5' /gb=R24723 /gi=779611 /ug=Hs.208543 /len=430	3.069508621	0.001131
84893_at	Cluster Incl. AI446168.ij07h07.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2140861 /clone_end=3' /gb=AI446168 /gi=4293320 /ug=Hs.176708 /len=435	3.066866421	0.023278
84612_at	Cluster Incl. AI864428.wf53a09.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2428600 /clone_end=3' /gb=AI864428 /gi=5528535 /ug=Hs.170880 /len=343	3.065443135	0.005335
73780_at	Cluster Incl. AA838748.ak03c10.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1404882 /clone_end=3' /gb=AA838748 /gi=2914860 /ug=Hs.123910 /len=543	3.06404637	0.009987
75705_at	Cluster Incl. AI634652.wa07e10.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2297418 /clone_end=3' /gb=AI634652 /gi=4685982 /ug=Hs.160795 /len=563	3.058453349	0.001904
70150_at	Cluster Incl. AI791593.oj57h03.y5 Homo sapiens cDNA, 5 end /clone=IMAGE-1502453 /clone_end=5' /gb=AI791593 /gi=5339309 /ug=Hs.203472 /len=472	3.050814176	0.000397
72125_at	Cluster Incl. N73802.yz80f05.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-289377 /clone_end=3' /gb=N73802 /gi=1231087 /ug=Hs.222824 /len=385	3.037955969	0.009677
75212_at	Cluster Incl. AI365208.qx97f11.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2010477 /clone_end=3' /gb=AI365208 /gi=4124897 /ug=Hs.138480 /len=291	3.027135566	0.003503
91678_at	Cluster Incl. AI814761.wk65d07.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2420269 /clone_end=3' /gb=AI814761 /gi=5425976 /ug=Hs.9204 /len=497	3.012896674	0.018287
90016_at	Cluster Incl. AI961177.wq59b09.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2475545 /clone_end=3' /gb=AI961177 /gi=5753890 /ug=Hs.124832 /len=835	3.00787812	0.013132

Table 6. U95_E Fold Change Genes (>3 over-expressed in Barrett's associated esophageal adenocarcinoma (BA), <0.33 under-expressed in BA)

Affy ID	Gene Name	Fold Change	P-value
73002_at	Cluster Incl. AI052526:oz27f09.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1676585 /clone_end=3' /gb=AI052526 /gi=3308517 /ug=Hs.233871 /len=290'	2.999558702	0.009676
90757_at	Cluster Incl. AI985612:wr75d05.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2493513 /clone_end=3' /gb=AI985612 /gi=5812889 /ug=Hs.184484 /len=486'	0.329081864	0.008916
78336_at	Cluster Incl. AI434477:ti37d01.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2132641 /clone_end=3' /gb=AI434477 /gi=4296452 /ug=Hs.210531 /len=421'	0.326191217	0.0046
73721_at	Cluster Incl. AA813527:ai67f11.s1 Homo sapiens cDNA, 3 end /clone=1375917 /clone_end=3' /gb=AA813527 /gi=2882212 /ug=Hs.122814 /len=459'	0.325630713	0.0109
72371_at	Cluster Incl. AI168188:oo09g11.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1565732 /clone_end=3' /gb=AI168188 /gi=3701358 /ug=Hs.225023 /len=448'	0.324150837	0.00589
71418_at	Cluster Incl. AI093188:qa98b05.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1694769 /clone_end=3' /gb=AI093188 /gi=3432164 /ug=Hs.215319 /len=471'	0.323684024	0.003636
86567_at	Cluster Incl. R19892:yg38f12.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-34798 /clone_end=5' /gb=R19892 /gi=774526 /ug=Hs.201458 /len=503'	0.320952495	0.00589
AFX-HS	X00351 Human mRNA for beta-actin (5, M, 3 represent transcript regions 5 prime, Middle, and 3 prime respectively)	0.320408458	0.004505
72290_r_a	Cluster Incl. AA814901:oa75g08.s1 Homo sapiens cDNA /clone=IMAGE-1318142 /gb=AA814901 /gi=2884497 /ug=Hs.224495 /len=459	0.320177197	0.042106
87950_at	Cluster Incl. AA313781:EST185644 Homo sapiens cDNA, 5 end /clone=ATCC-109963 /clone_end=5' /gb=AA313781 /gi=1966110 /ug=Hs.236903 /len=599'	0.320113508	0.001602
91014_at	Cluster Incl. N23781:yx35e09.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-263752 /clone_end=5' /gb=N23781 /gi=1137931 /ug=Hs.226614 /len=592'	0.31964593	0.028338
70650_at	Cluster Incl. AA779712:af43h05.s1 Homo sapiens cDNA, 3 end /clone=1034457 /clone_end=3' /gb=AA779712 /gi=2839043 /ug=Hs.208718 /len=606'	0.318766299	0.010363
69829_at	Cluster Incl. AI684559:wa84a03.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2302828 /clone_end=3' /gb=AI684559 /gi=4895853 /ug=Hs.201637 /len=507'	0.315917401	0.020149
91462_at	Cluster Incl. W26201:22c1 Homo sapiens cDNA /gb=W26201 /gi=1306612 /ug=Hs.183793 /len=470	0.315659043	0.00959
84412_at	Cluster Incl. AI525044:promna-5.C09.r Homo sapiens cDNA, 5 end /clone_end=5' /gb=AI525044 /gi=4439179 /ug=Hs.168007 /len=639'	0.313783504	0.009654

Table 6. U95_E Fold Change Genes (>3 over-expressed in Barrett's associated esophageal adenocarcinoma (BA), <0.33 under-expressed in BA)

Affy ID	Gene Name	Fold Change	P-value
78228_s	Cluster Incl. A1561042:tg29e02.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2210234 /clone_end=3' /gb=A1561042 /gi=4511383 /ug=Hs.239771 /len=635'	0.312957775	0.008401
67280_at	Cluster Incl. A1243125:qh26h01.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1845841 /clone_end=3' /gb=A1243125 /gi=3838522 /ug=Hs.182947 /len=388'	0.312853457	0.03165
72558_at	Cluster Incl. A1858718:wi41f12.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2427503 /clone_end=3' /gb=A1858718 /gi=5512334 /ug=Hs.226562 /len=654'	0.312511549	0.014896
76043_at	Cluster Incl. AW015534:Ul-H-B10p-aa-b-12-O-Ul.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-2710606 /clone_end=3' /gb=AW015534 /gi=5864281 /ug=Hs.234248 /len=519'	0.312460844	0.007489
84991_at	Cluster Incl. A1732539:ni01f09.x5 Homo sapiens cDNA, 3 end /clone=IMAGE-966761 /clone_end=3' /gb=A1732539 /gi=5053652 /ug=Hs.180142 /len=508'	0.31169073	0.040979
71283_at	Cluster Incl. R35259:yg61b10.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-37315 /clone_end=5' /gb=R35259 /gi=792160 /ug=Hs.213548 /len=513'	0.311634623	0.000087
79909_l_a	Cluster Incl. A1808615:wf56f01.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2359609 /clone_end=3' /gb=A1808615 /gi=5395181 /ug=Hs.202625 /len=443'	0.310115615	0.000765
84081_at	Cluster Incl. A1420234:te98b01.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2094697 /clone_end=3' /gb=A1420234 /gi=4266165 /ug=Hs.163645 /len=501'	0.309511353	0.000025
83406_at	Cluster Incl. A1935292:wp16e07.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2465028 /clone_end=3' /gb=A1935292 /gi=5674162 /ug=Hs.153408 /len=573'	0.307974308	0.006092
68268_at	Cluster Incl. AA702143:zi85h05.s1 Homo sapiens cDNA, 3 end /clone=447609 /clone_end=3' /gb=AA702143 /gi=2705256 /ug=Hs.190365 /len=447'	0.30729455	0.027087
84950_at	Cluster Incl. A1681868:bx50a12.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2272990 /clone_end=3' /gb=A1681868 /gi=4892050 /ug=Hs.178784 /len=562'	0.304600093	0.000743
71416_at	Cluster Incl. A1023259:ov64g12.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1642150 /clone_end=3' /gb=A1023259 /gi=3238500 /ug=Hs.215260 /len=501'	0.303909365	0.000025
79484_r_a	Cluster Incl. N73382:EST55b03 Homo sapiens cDNA /clone=55b03 /gb=N73382 /gi=1230490 /ug=Hs.193146 /len=398	0.303863976	0.033101
76752_at	Cluster Incl. A1653380:wb45d09.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2308625 /clone_end=3' /gb=A1653380 /gi=4737359 /ug=Hs.133081 /len=517'	0.30383599	0.00007

Table 6. U95_E Fold Change Genes (>3 over-expressed in Barrett's associated esophageal adenocarcinoma (BA), <0.33 under-expressed in BA)

Affy ID	Gene Name	Fold Change	P-value
88480_at	Cluster Incl. AI076929:ov20f07.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1637893 /clone_end=3' /gb=AI076929 /gi=3404758 /ug=Hs.105887 /len=589'	0.303580242	0.04562
76056_at	Cluster Incl. AA161405:zo72g08.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-592478 /clone_end=5' /gb=AA161405 /gi=1735835 /ug=Hs.237871 /len=666'	0.301518123	0.016888
84827_at	Cluster Incl. H45983:yo13b04.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-177775 /clone_end=3' /gb=H45983 /gi=922035 /ug=Hs.174198 /len=485'	0.299353312	0.004482
91207_at	Cluster Incl. AA923142:gi=3070451 /ug=Hs.24884 /len=653'	0.294579992	0.002012
81631_at	Cluster Incl. AW007764:wf68h01.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2512657 /clone_end=3' /gb=AW007764 /gi=5856542 /ug=Hs.121915 /len=516'	0.294066245	0.024164
90059_at	Cluster Incl. AI921788:wn65c05.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2450312 /clone_end=3' /gb=AI921788 /gi=5657752 /ug=Hs.126082 /len=550'	0.292038446	0.000325
71426_f_a	Cluster Incl. AI277946:qm51b03.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1892237 /clone_end=3' /gb=AI277946 /gi=3900214 /ug=Hs.215571 /len=334'	0.291075799	0.005808
81951_at	Cluster Incl. AI640180:wa30a12.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2299582 /clone_end=3' /gb=AI640180 /gi=4703289 /ug=Hs.126855 /len=463'	0.291050583	0.003823
70677_at	Cluster Incl. AI783611:tz99c01.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2296704 /clone_end=3' /gb=AI783611 /gi=5325420 /ug=Hs.208907 /len=325'	0.290005448	0.027407
79507_r_a	Cluster Incl. AA180065:zp40h07.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-611965 /clone_end=3' /gb=AA180065 /gi=1761331 /ug=Hs.193579 /len=438'	0.289433499	0.01687
86556_at	Cluster Incl. AI769511:wh57h04.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2384887 /clone_end=3' /gb=AI769511 /gi=5236020 /ug=Hs.201259 /len=550'	0.288562177	0.00028
75652_at	Cluster Incl. AI983437:wf49b04.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2510767 /clone_end=3' /gb=AI983437 /gi=5810656 /ug=Hs.155145 /len=504'	0.28652751	0.006637
84975_r_a	Cluster Incl. AA649608:ns46b02.s1 Homo sapiens cDNA /clone=IMAGE-1186635 /gb=AA649608 /gi=2576936 /ug=Hs.179821 /len=316'	0.28641313	0.000038
80632_at	Cluster Incl. AA846471:aj56d07.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1394317 /clone_end=3' /gb=AA846471 /gi=2932611 /ug=Hs.239354 /len=643'	0.286244603	0.007418

Table 6. U95_E Fold Change Genes (>3 over-expressed in Barrett's associated esophageal adenocarcinoma (BA), <0.33 under-expressed in BA)

Affy ID	Gene Name	Fold Change	P-value
70813_at	Cluster Incl. AI797429:we54c10.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2344914 /clone_end=3' /gb=AI797429 /gi=5362901 /ug=Hs.209518 /len=357'	0.285905069	0.001632
76199_at	Cluster Incl. AA057583:zf62e12.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-381550 /clone_end=3' /gb=AA057583 /gi=1550223 /ug=Hs.118553 /len=524'	0.285315234	0.000117
72405_at	Cluster Incl. AI948717:wq25a02.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2472266 /clone_end=3' /gb=AI948717 /gi=5741027 /ug=Hs.225155 /len=505'	0.28501066	0.003409
74580_at	Cluster Incl. AA417643:zv04a08.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-752630 /clone_end=5' /gb=AA417643 /gi=2079462 /ug=Hs.130546 /len=490'	0.284080797	0.006142
77399_at	Cluster Incl. AI361798:qz24f08.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2027847 /clone_end=3' /gb=AI361798 /gi=4113419 /ug=Hs.164675 /len=541'	0.282876221	0.009253
78543_at	Cluster Incl. AA877572:nr05g06.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1160986 /clone_end=3' /gb=AA877572 /gi=2986537 /ug=Hs.155512 /len=429'	0.282804511	0.002194
69157_at	Cluster Incl. AI651803:wb55f04.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2309599 /clone_end=3' /gb=AI651803 /gi=4735794 /ug=Hs.195264 /len=359'	0.277835487	0.001605
86353_at	Cluster Incl. AI767724:wh39a07.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2383092 /clone_end=3' /gb=AI767724 /gi=5234233 /ug=Hs.197287 /len=556'	0.276458086	0.000703
89837_r_a	Cluster Incl. T89638:ye11d12.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-117431 /clone_end=3' /gb=T89638 /gi=718151 /ug=Hs.116792 /len=517'	0.275506295	0.007145
86050_at	Cluster Incl. AA213912:zn57h11.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-562341 /clone_end=3' /gb=AA213912 /gi=1812714 /ug=Hs.193564 /len=544'	0.274761317	0.000129
91748_at	Cluster Incl. W68223:zd35c12.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-342646 /clone_end=5' /gb=W68223 /gi=1377161 /ug=Hs.238901 /len=609'	0.273530639	0.043603
86004_at	Cluster Incl. AA767895:oa40a11.s1 Homo sapiens cDNA /clone=IMAGE-1307420 /gb=AA767895 /gi=2818910 /ug=Hs.193247 /len=538	0.273401061	0.000134
87972_s	Cluster Incl. AW023444:df54h10.y1 Homo sapiens cDNA, 5 end /clone=IMAGE-2487403 /clone_end=5' /gb=AW023444 /gi=5876974 /ug=Hs.237396 /len=465'	0.271780784	0.000549
82088_at	Cluster Incl. H24953:yj39f08.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-160647 /clone_end=3' /gb=H24953 /gi=893852 /ug=Hs.130815 /len=529'	0.271229201	0.006574

Table 6. U95_E Fold Change Genes (>3 over-expressed in Barrett's associated esophageal adenocarcinoma (BA), <0.33 under-expressed in BA)

Affy ID	Gene Name	Fold Change	P-value
86204_at	Cluster Incl. AI827476/wf29g07.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2357052 /clone_end=3' /gb=AI827476 /gi=5448147 /ug=Hs.194421 /len=520'	0.269758658	0.019109
90088_at	Cluster Incl. AI807902/wf52b01.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2359177 /clone_end=3' /gb=AI807902 /gi=5394468 /ug=Hs.127301 /len=554'	0.269431153	0.001195
73728_at	Cluster Incl. AI073865/oo12a05.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1565936 /clone_end=3' /gb=AI073865 /gi=3400509 /ug=Hs.122821 /len=458'	0.269254487	0.004875
89656_at	Cluster Incl. R53734/yf02g05.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-138104 /clone_end=5' /gb=R53734 /gi=815636 /ug=Hs.25978 /len=430'	0.268646481	0.005615
71466_at	Cluster Incl. AI453103/tj61f03.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2146013 /clone_end=3' /gb=AI453103 /gi=4308016 /ug=Hs.216699 /len=481'	0.267307121	0.034897
81596_at	Cluster Incl. AI694593/wd88f10.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2338699 /clone_end=3' /gb=AI694593 /gi=4971933 /ug=Hs.121574 /len=538'	0.266846366	0.009889
87152_at	Cluster Incl. AA554814/nl34c04.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-978726 /clone_end=3' /gb=AA554814 /gi=2325353 /ug=Hs.213551 /len=443'	0.265915547	0.017712
83897_at	Cluster Incl. AI458439/tj82c11.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2148020 /clone_end=3' /gb=AI458439 /gi=4311018 /ug=Hs.159115 /len=557'	0.26411577	0.000037
77613_at	Cluster Incl. R54310/yg74a09.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-38941 /clone_end=5' /gb=R54310 /gi=816212 /ug=Hs.18685 /len=522'	0.262617018	0.014534
81862_at	Cluster Incl. AI138884/qd99c07.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1737612 /clone_end=3' /gb=AI138884 /gi=3644856 /ug=Hs.125490 /len=482'	0.262322708	0.048252
87927_at	Cluster Incl. AW003850/ws61b04.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2501647 /clone_end=3' /gb=AW003850 /gi=5850766 /ug=Hs.236664 /len=562'	0.26115592	0.002756
86211_at	Cluster Incl. AI621034/ts76b11.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2237181 /clone_end=3' /gb=AI621034 /gi=4630160 /ug=Hs.194449 /len=556'	0.261152746	0.033787
88019_f_a	Cluster Incl. AI968388/wu02e09.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2515816 /clone_end=3' /gb=AI968388 /gi=5765206 /ug=Hs.238114 /len=301'	0.259572265	0.049172
AFFX-HU	M33197 Human glyceraldehyde-3-phosphate dehydrogenase (GAPDH) mRNA, complete cds (5, _M, _3 represent transcript regions 5 prime, Middle, and 3 prime respectively)	0.257980182	0.015423

Table 6. U95_E Fold Change Genes (>3 over-expressed in Barrett's associated esophageal adenocarcinoma (BA), <0.33 under-expressed in BA)

Affy ID	Gene Name	Fold Change	P-value
77773_at	Cluster Incl. AA593528:nn28a06.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1085170 /clone_end=3' /gb=AA593528 /gi=2409290 /ug=Hs.198976 /len=433'	0.2562359	0.028242
85360_at	Cluster Incl. AA255965:zs28g07.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-686556 /clone_end=3' /gb=AA255965 /gi=1891523 /ug=Hs.186853 /len=406'	0.255474175	0.006366
76212_at	Cluster Incl. W26941:16f10 Homo sapiens cDNA /gb=W26941 /gi=1306169 /ug=Hs.118727 /len=547	0.255231274	0.000598
90585_at	Cluster Incl. AI368415:qy08b11.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2011389 /clone_end=3' /gb=AI368415 /gi=4147168 /ug=Hs.155074 /len=759'	0.25397395	0.006918
67405_at	Cluster Incl. AI610167:tp13h07.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2187709 /clone_end=3' /gb=AI610167 /gi=4619334 /ug=Hs.185056 /len=567'	0.253224559	0.005829
86842_at	Cluster Incl. W06950:za91a12.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-299902 /clone_end=5' /gb=W06950 /gi=1280952 /ug=Hs.206454 /len=523'	0.252673195	0.001281
82083_at	Cluster Incl. AA903403:ok62c08.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1518542 /clone_end=3' /gb=AA903403 /gi=3038526 /ug=Hs.130761 /len=551'	0.252499158	0.002692
67461_at	Cluster Incl. AA702220:zi84e01.s1 Homo sapiens cDNA, 3 end /clone=447480 /clone_end=3' /gb=AA702220 /gi=2705333 /ug=Hs.185783 /len=462'	0.252109936	0.002038
80797_at	Cluster Incl. AL044128:DKFZp434N0628.s1 Homo sapiens cDNA, 3 end /clone=DKFZp434N0628 /clone_end=3' /gb=AL044128 /gi=5432354 /ug=Hs.94195 /len=983'	0.251370696	0.000508
81053_at	Cluster Incl. AI273624:qj56c06.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1876330 /clone_end=3' /gb=AI273624 /gi=3895892 /ug=Hs.115192 /len=414'	0.249890723	0.000955
77218_at	Cluster Incl. AA634799:ab28b06.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-842099 /clone_end=5' /gb=AA634799 /gi=2558013 /ug=Hs.151888 /len=538'	0.249121821	0.000134
79663_at	Cluster Incl. AI566193:tp69f02.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2214075 /clone_end=3' /gb=AI566193 /gi=4524645 /ug=Hs.196927 /len=393'	0.249088172	0.035959
85962_at	Cluster Incl. AI923659:wn59b05.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2449713 /clone_end=3' /gb=AI923659 /gi=5659623 /ug=Hs.192972 /len=577'	0.247682275	0.00136
83951_r a	Cluster Incl. AA812024:ob39g08.s1 Homo sapiens cDNA /clone=IMAGE-1333790 /gb=AA812024 /gi=2881635 /ug=Hs.159669 /len=410	0.243142897	0.009508
78463_at	Cluster Incl. AI160540:qc87a04.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1721166 /clone_end=3' /gb=AI160540 /gi=3693920 /ug=Hs.13781 /len=579'	0.242819085	0.017392

Table 6. U95_E Fold Change Genes (>3 over-expressed in Barrett's associated esophageal adenocarcinoma (BA), <0.33 under-expressed in BA)

Affy ID	Gene Name	Fold Change	P-value
84535_at	Cluster Incl. N50065:yz10h03.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-282677 /clone_end=3' /gb=N50065 /gi=1191231 /ug=Hs.169732 /len=550'	0.242621323	0.040681
91147_at	Cluster Incl. AI929144:au65f04.y1 Homo sapiens cDNA /clone=IMAGE /gb=AI929144 /gi=5665108 /ug=Hs.239175 /len=724	0.241886973	0.000589
80851_at	Cluster Incl. AI733027:oj14a06.x5 Homo sapiens cDNA, 3 end /clone=IMAGE-1492114 /clone_end=3' /gb=AI733027 /gi=5054140 /ug=Hs.105206 /len=590'	0.241842162	0.000183
91750_at	Cluster Incl. AI921883:wp07f05.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2464161 /clone_end=3' /gb=AI921883 /gi=5657847 /ug=Hs.23921 /len=582'	0.234701355	0.000625
74161_at	Cluster Incl. AA960997:oo51f06.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1569731 /clone_end=3' /gb=AA960997 /gi=3127551 /ug=Hs.127765 /len=434'	0.234459062	0.005177
90373_r_a	Cluster Incl. N54525:yy37d07.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-244909 /clone_end=3' /gb=N54525 /gi=1195845 /ug=Hs.141278 /len=495'	0.2338597	0
86687_i_a	Cluster Incl. AI885491:wm24f11.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2436909 /clone_end=3' /gb=AI885491 /gi=5590655 /ug=Hs.203196 /len=464'	0.233577442	0.000091
76769_at	Cluster Incl. AI758223:ty66b04.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2284015 /clone_end=3' /gb=AI758223 /gi=5151946 /ug=Hs.133471 /len=535'	0.233395219	0.000097
73026_s	Cluster Incl. AI420118:tf05b01.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2095273 /clone_end=3' /gb=AI420118 /gi=4266049 /ug=Hs.234008 /len=429'	0.22622915	0.035572
91887_f_a	Cluster Incl. AI860139:wh39f08.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2383143 /clone_end=3' /gb=AI860139 /gi=5513755 /ug=Hs.134556 /len=528'	0.225862338	0.001895
81686_at	Cluster Incl. AA807273:oc33e01.s1 Homo sapiens cDNA /clone=IMAGE-1351512 /gb=AA807273 /gi=2876849 /ug=Hs.122832 /len=469	0.221895364	0.030677
78622_r_a	Cluster Incl. W26589:33d9 Homo sapiens cDNA /gb=W26589 /gi=1307432 /ug=Hs.22954 /len=594	0.221208606	0.003353
89844_at	Cluster Incl. AI806507:wf08h01.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2350033 /clone_end=3' /gb=AI806507 /gi=5393073 /ug=Hs.117772 /len=565'	0.219504698	0.001214
76942_i_a	Cluster Incl. AI821447:yp24d10.x5 Homo sapiens cDNA, 3 end /clone=IMAGE-188371 /clone_end=3' /gb=AI821447 /gi=5440526 /ug=Hs.141120 /len=542'	0.218832459	0.00729
82865_at	Cluster Incl. AI829717:wf09f05.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2350113 /clone_end=3' /gb=AI829717 /gi=5450388 /ug=Hs.146016 /len=541'	0.218261577	0.006778

Table 6. U95_E Fold Change Genes (>3 over-expressed in Barrett's associated esophageal adenocarcinoma (BA), <0.33 under-expressed in BA)

Affy ID	Gene Name	Fold Change	P-value
90629_at	Cluster Incl. X84721:HSEST222 Homo sapiens cDNA /clone=MEC-222 /gb=X84721 /gi=673398 /ug=Hs.164866 /len=558	0.21759462	0.018709
78209_at	Cluster Incl. T79705:yd71e10.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-113706 /clone_end=5' /gb=T79705 /gi=698214 /ug=Hs.239664 /len=453'	0.217378721	0.0002
89338_at	Cluster Incl. AA102335:z191b05.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-511953 /clone_end=3' /gb=AA102335 /gi=1647042 /ug=Hs.183620 /len=540'	0.216876929	0.011804
87935_r_a	Cluster Incl. A1817659:td15b09.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2075705 /clone_end=3' /gb=A1817659 /gi=5436738 /ug=Hs.236720 /len=457'	0.216095926	0.001085
90111_at	Cluster Incl. A1417537:tg79c03.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2114980 /clone_end=3' /gb=A1417537 /gi=4261041 /ug=Hs.127808 /len=512'	0.214818394	0.03032
88754_at	Cluster Incl. AA775833:ad17c09.s1 Homo sapiens cDNA, 3 end /clone=878512 /clone_end=3' /gb=AA775833 /gi=2835167 /ug=Hs.122655 /len=501'	0.210857155	0.040755
71736_at	Cluster Incl. AA937952:oc08c08.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1340270 /clone_end=3' /gb=AA937952 /gi=3096063 /ug=Hs.221237 /len=373'	0.206013142	0.000046
79489_at	Cluster Incl. A1620433:tu47b05.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2254161 /clone_end=3' /gb=A1620433 /gi=4629559 /ug=Hs.193201 /len=486'	0.205729323	0.001955
89360_at	Cluster Incl. AA630327:ac08g11.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-855908 /clone_end=3' /gb=AA630327 /gi=2552938 /ug=Hs.185158 /len=637'	0.20325397	0.003
91460_at	Cluster Incl. A1342616:q133e02.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1949786 /clone_end=3' /gb=A1342616 /gi=4079543 /ug=Hs.183793 /len=471'	0.200209939	0.037457
76759_r_a	Cluster Incl. A1224653:qw97g08.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1999070 /clone_end=3' /gb=A1224653 /gi=3807366 /ug=Hs.133286 /len=448'	0.196540489	0.000067
84240_at	Cluster Incl. W93868:zd97a07.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-357396 /clone_end=5' /gb=W93868 /gi=1423010 /ug=Hs.166241 /len=426'	0.196285806	0.003331
71069_at	Cluster Incl. A1832201:td14b10.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2075611 /clone_end=3' /gb=A1832201 /gi=5452872 /ug=Hs.211469 /len=475'	0.195317324	0.002561
85168_at	Cluster Incl. A1653441:tg94b09.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2216441 /clone_end=3' /gb=A1653441 /gi=4737420 /ug=Hs.183409 /len=448'	0.193174439	0.000276

Table 6. U95_E Fold Change Genes (>3 over-expressed in Barrett's associated esophageal adenocarcinoma (BA), <0.33 under-expressed in BA)

Affy ID	Gene Name	Fold Change	P-value
73285_i_a	Cluster Incl. AI971748:wr07f08.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2480871 /clone_end=3' /gb=AI971748 /gi=5768574 /ug=Hs.236704 /len=841'	0.185052334	0.002302
91306_s	Cluster Incl. AA613715:nq25b01.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1144873 /clone_end=3' /gb=AA613715 /gi=2463685 /ug=Hs.81795 /len=607'	0.184479141	0.000085
91309_r_a	Cluster Incl. AA613715:nq25b01.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1144873 /clone_end=3' /gb=AA613715 /gi=2463685 /ug=Hs.81795 /len=607'	0.180034385	0.000184
77736_at	Cluster Incl. AA604618:nc84b05.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1113489 /clone_end=3' /gb=AA604618 /gi=2445482 /ug=Hs.194090 /len=437'	0.178791804	0.000087
67440_r_a	Cluster Incl. AA419260:zv35c03.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-755620 /clone_end=3' /gb=AA419260 /gi=2078973 /ug=Hs.185665 /len=456'	0.176702997	0.015013
82862_at	Cluster Incl. AI817698:wk25b08.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2413335 /clone_end=3' /gb=AI817698 /gi=5436777 /ug=Hs.145994 /len=548'	0.176441557	0.036843
72186_at	Cluster Incl. AI580176:tk17g08.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2151326 /clone_end=3' /gb=AI580176 /gi=4564552 /ug=Hs.223394 /len=513'	0.175060418	0.005973
87011_at	Cluster Incl. AI040273:ox92d10.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1663795 /clone_end=3' /gb=AI040273 /gi=3279467 /ug=Hs.210508 /len=450'	0.174753613	0.016883
67117_at	Cluster Incl. AA026238:zj99f11.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-469197 /clone_end=3' /gb=AA026238 /gi=1492777 /ug=Hs.181272 /len=395'	0.174410782	0.003724
72418_r_a	Cluster Incl. AI990292:ws30h05.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2498745 /clone_end=3' /gb=AI990292 /gi=5837173 /ug=Hs.225457 /len=445'	0.172944529	0.001836
76618_at	Cluster Incl. AI806805:wf15e07.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2350692 /clone_end=3' /gb=AI806805 /gi=5393371 /ug=Hs.129965 /len=487'	0.171672809	0.004788
74321_at	Cluster Incl. AI702482:tz94e07.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2296260 /clone_end=3' /gb=AI702482 /gi=4990382 /ug=Hs.128672 /len=494'	0.165834292	0.003435
71946_at	Cluster Incl. AI005278:ou07g04.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1625622 /clone_end=3' /gb=AI005278 /gi=3214788 /ug=Hs.222140 /len=481'	0.165484982	0.002113
91356_at	Cluster Incl. AI392846:tg10d02.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2108355 /clone_end=3' /gb=AI392846 /gi=4222393 /ug=Hs.95744 /len=542'	0.164854129	0.005954

Table 6. U95_E Fold Change Genes (>3 over-expressed in Barrett's associated esophageal adenocarcinoma (BA), <0.33 under-expressed in BA)

Affy ID	Gene Name	Fold Change	P-value
85092_g	Cluster Incl. A1554809:tp73f01.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2204953 /clone_end=3' /gb=A1554809 /gi=4487172 /ug=Hs.182339 /len=1035'	0.164014819	0.000531
91414_at	Cluster Incl. N72573:za46c03.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-295588 /clone_end=3' /gb=N72573 /gi=1229677 /ug=Hs.118183 /len=482'	0.16120887	0.005273
86418_at	Cluster Incl. A1978581:wq72d08.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2476815 /clone_end=3' /gb=A1978581 /gi=5803611 /ug=Hs.198694 /len=475'	0.160027369	0.000057
86370_at	Cluster Incl. AW003775:ws16h04.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2497399 /clone_end=3' /gb=AW003775 /gi=5850691 /ug=Hs.197737 /len=647'	0.159738807	0.015431
83047_at	Cluster Incl. A1627358:ty75d11.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2284917 /clone_end=3' /gb=A1627358 /gi=4664158 /ug=Hs.148367 /len=552'	0.158131021	0.016115
89805_at	Cluster Incl. A1568633:tn41f11.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2170221 /clone_end=3' /gb=A1568633 /gi=4532007 /ug=Hs.114670 /len=481'	0.157868321	0.000963
68787_at	Cluster Incl. AA682328:zj98d05.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-462921 /clone_end=3' /gb=AA682328 /gi=2669645 /ug=Hs.193084 /len=484'	0.157814866	0.016057
75096_at	Cluster Incl. AA769588:nz42b06.s1 Homo sapiens cDNA /clone=IMAGE-1290419 /gb=AA769588 /gi=2820826 /ug=Hs.135723 /len=607'	0.156801675	0.003643
86085_r_a	Cluster Incl. AA419311:zv35c03.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-755620 /clone_end=5' /gb=AA419311 /gi=2079024 /ug=Hs.193745 /len=690'	0.154848601	0.002758
77356_at	Cluster Incl. AL110434:DKFZp434N1031_r1 Homo sapiens cDNA, 5 end /clone=DKFZp434N1031 /clone_end=5' /gb=AL110434 /gi=5866042 /ug=Hs.162685 /len=638'	0.153135161	0.002875
86396_at	Cluster Incl. AW001450:wu31f11.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-990784 /clone_end=3' /gb=AW001450 /gi=5848366 /ug=Hs.198312 /len=517'	0.153122052	0.002676
73425_at	Cluster Incl. A1971458:wq86e05.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2478944 /clone_end=3' /gb=A1971458 /gi=5768284 /ug=Hs.239145 /len=513'	0.152644343	0.005367
67222_at	Cluster Incl. A1219734:qg88c02.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1842242 /clone_end=3' /gb=A1219734 /gi=3801937 /ug=Hs.182221 /len=443'	0.147483257	0.000055
81926_at	Cluster Incl. A1685069:wc67b06.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2323667 /clone_end=3' /gb=A1685069 /gi=4896374 /ug=Hs.126383 /len=504'	0.143799679	0.001664

Table 6. U95_E Fold Change Genes (>3 over-expressed in Barrett's associated esophageal adenocarcinoma (BA), <0.33 under-expressed in BA)

Affy ID	Gene Name	Fold Change	P-value
79554_at	Cluster Incl. H97871.yw05a04.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-251310 /clone_end=3' /gb=H97871 /gi=1118756 /ug=Hs.193907 /len=445'	0.141155538	0.000118
70209_at	Cluster Incl. A1761629.wg66g02.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2370098 /clone_end=3' /gb=A1761629 /gi=51177296 /ug=Hs.203696 /len=535'	0.140186121	0.000424
80602_at	Cluster Incl. AW003595.wx34a07.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2545524 /clone_end=3' /gb=AW003595 /gi=5850511 /ug=Hs.239177 /len=586'	0.131039201	0.004556
91072_at	Cluster Incl. R78708.yj74a09.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-144952 /clone_end=5' /gb=R78708 /gi=854989 /ug=Hs.237163 /len=588'	0.126447658	0.000068
91826_at	Cluster Incl. A1219073.qg16e08.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1759718 /clone_end=3' /gb=A1219073 /gi=3801276 /ug=Hs.126062 /len=555'	0.123573477	0.02356
88725_at	Cluster Incl. AA622392.no45c05.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1103624 /clone_end=3' /gb=AA622392 /gi=2526268 /ug=Hs.122244 /len=503'	0.12192783	0.007314
77982_at	Cluster Incl. A1820925.zu53f08.y5 Homo sapiens cDNA, 5 end /clone=IMAGE-741735 /clone_end=5' /gb=A1820925 /gi=5440004 /ug=Hs.227048 /len=600'	0.120125995	0.000268
78295_r_a	Cluster Incl. A1733324.op02a10.x5 Homo sapiens cDNA, 3 end /clone=IMAGE-1574490 /clone_end=3' /gb=A1733324 /gi=5054437 /ug=Hs.57138 /len=500'	0.11926614	0.009
84128_at	Cluster Incl. A1434862.ti13c03.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2130340 /clone_end=3' /gb=A1434862 /gi=4299148 /ug=Hs.164224 /len=391'	0.11733946	0.001254
76068_at	Cluster Incl. A1819863.wj45h05.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2405817 /clone_end=3' /gb=A1819863 /gi=5438942 /ug=Hs.106243 /len=612'	0.109228797	0.001154
76847_at	Cluster Incl. A1951161.wx64c08.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2548430 /clone_end=3' /gb=A1951161 /gi=5743471 /ug=Hs.135184 /len=451'	0.106139272	0.000562
86083_i_a	Cluster Incl. AA419311.zv35c03.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-755620 /clone_end=5' /gb=AA419311 /gi=2079024 /ug=Hs.193745 /len=690'	0.105672634	0.00005
89807_at	Cluster Incl. A1418405.tg36e10.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2110890 /clone_end=3' /gb=A1418405 /gi=4264336 /ug=Hs.115173 /len=472'	0.105567733	0.002877
69815_at	Cluster Incl. A1684761.wa85h04.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2302999 /clone_end=3' /gb=A1684761 /gi=4896055 /ug=Hs.201552 /len=678'	0.105063837	0.002168

Table 6. U95_E Fold Change Genes (>3 over-expressed in Barrett's associated esophageal adenocarcinoma (BA), <0.33 under-expressed in BA)

Affy ID	Gene Name	Fold Change	P-value
79447_at	Cluster Incl. A1452552:ij62h11.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2146149 /clone_end=3' /gb=A1452552 /gi=4286151 /ug=Hs.192825 /len=398'	0.102930746	0
74723_at	Cluster Incl. A1375142:tc09h05.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2063385 /clone_end=3' /gb=A1375142 /gi=4175132 /ug=Hs.132127 /len=458'	0.10188118	0.000018
87275_at	Cluster Incl. AA190398:zp86g11.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-627140 /clone_end=3' /gb=AA190398 /gi=1779348 /ug=Hs.220905 /len=570'	0.098256541	0.000886
81445_at	Cluster Incl. AA830533:oc52c05.s1 Homo sapiens cDNA /clone=IMAGE-1353320 /gb=AA830533 /gi=2903632 /ug=Hs.120219 /len=426'	0.095034843	0.000324
85093_at	Cluster Incl. A1991109:wu38c03.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-991031 /clone_end=3' /gb=A1991109 /gi=5838012 /ug=Hs.182339 /len=832'	0.090173646	0.001181
80411_g	Cluster Incl. AA961504:op44f07.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1579717 /clone_end=3' /gb=AA961504 /gi=3133668 /ug=Hs.234808 /len=473'	0.082703596	0.000614
86688_f a	Cluster Incl. A1885491:wm24f11.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2436909 /clone_end=3' /gb=A1885491 /gi=5590655 /ug=Hs.203196 /len=464'	0.080705969	0.000529
83638_at	Cluster Incl. A1570023:fr91b11.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2226429 /clone_end=3' /gb=A1570023 /gi=4533397 /ug=Hs.156457 /len=401'	0.076248907	0.001755
84121_at	Cluster Incl. A1480137:fm33f01.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2159929 /clone_end=3' /gb=A1480137 /gi=4373305 /ug=Hs.164198 /len=558'	0.070707403	0.000394
72187_g	Cluster Incl. A1580176:lk17g08.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2151326 /clone_end=3' /gb=A1580176 /gi=4564552 /ug=Hs.223394 /len=513'	0.07033885	0.000099
74335_at	Cluster Incl. A1950844:wx55h06.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2547611 /clone_end=3' /gb=A1950844 /gi=5743154 /ug=Hs.128738 /len=426'	0.062942854	0.000823
74168_at	Cluster Incl. A1859619:wm14d07.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2435917 /clone_end=3' /gb=A1859619 /gi=5513235 /ug=Hs.127780 /len=525'	0.062714223	0.000097
75414_at	Cluster Incl. AA897501:aj62a04.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1394862 /clone_end=3' /gb=AA897501 /gi=3034121 /ug=Hs.143529 /len=504'	0.061379361	0
81956_at	Cluster Incl. A1459244:tk11d02.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2150691 /clone_end=3' /gb=A1459244 /gi=4311823 /ug=Hs.126897 /len=489'	0.060318825	0.000092

Table 6. U95_E Fold Change Genes (>3 over-expressed in Barrett's associated esophageal adenocarcinoma (BA), <0.33 under-expressed in BA)

Affy ID	Gene Name	Fold Change	P-value
80408_at	Cluster Incl. AA961504:op44f07.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1579717 /clone_end=3' /gb=AA961504 /gi=3133668 /ug=Hs.234808 /len=473'	0.058236213	0.002633
91978_r_a	Cluster Incl. AI457596:tfj63b09.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2146169 /clone_end=3' /gb=AI457596 /gi=4310465 /ug=Hs.204169 /len=513'	0.057105024	0
88237_s	Cluster Incl. AA490688:aa45b06.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-823859 /clone_end=5' /gb=AA490688 /gi=2219861 /ug=Hs.239723 /len=561'	0.056521395	0.000735
83425_at	Cluster Incl. AI739630:wi37d03.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2392421 /clone_end=3' /gb=AI739630 /gi=5101611 /ug=Hs.153590 /len=461'	0.050662272	0
89468_at	Cluster Incl. AA614254:np09h02.s1 Homo sapiens cDNA /clone=IMAGE-1115859 /gb=AA614254 /gi=2466388 /ug=Hs.200539 /len=468	0.048326422	0.000573
70495_at	Cluster Incl. AI453095:tfj52e10.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2145162 /clone_end=3' /gb=AI453095 /gi=4307387 /ug=Hs.207393 /len=555'	0.047278322	0.000031
67146_l_a	Cluster Incl. AI349119:ta51g03.x2 Homo sapiens cDNA, 3 end /clone=IMAGE-2047636 /clone_end=3' /gb=AI349119 /gi=4086325 /ug=Hs.181625 /len=114'	0.04516733	0
82818_at	Cluster Incl. AI733800:qk36c08.x5 Homo sapiens cDNA, 3 end /clone=IMAGE-1871054 /clone_end=3' /gb=AI733800 /gi=5054913 /ug=Hs.145582 /len=489'	0.042193449	0.000056
76345_r_a	Cluster Incl. AA843931:ai90g08.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-1388126 /clone_end=3' /gb=AA843931 /gi=2930382 /ug=Hs.124221 /len=493'	0.037828358	0.000112
78159_s	Cluster Incl. AI582193:tg63e12.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2213518 /clone_end=3' /gb=AI582193 /gi=4568090 /ug=Hs.239207 /len=461'	0.028462315	0.000001
75060_at	Cluster Incl. AI814274:wj71a06.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2408242 /clone_end=3' /gb=AI814274 /gi=5425489 /ug=Hs.135188 /len=499'	0.008079595	0.000572

Table 7. Genes present in the U95_A cluster which are not in the Fold Change list (>1 over-expressed in Barrett's-associated esophageal denocarcinoma (BA), <1 under-expressed in BA)

Affy ID	Gene Name	Fold Change	P-value
760_at	Y09216 /FEATURE= /DEFINITION=HSDYRK2 H.sapiens mRNA for protein kinase, Dyk2	1.776710327	0.029598
39260_at	Cluster Incl U59185:Human putative monocarboxylate transporter (MCT) mRNA, complete cds /cds=(182,1645) /gb=U59185 /gi=2463627 /ug=Hs.23590 /len=2529	1.853453277	0.020819
35219_at	Cluster Incl AL050202:Homo sapiens mRNA; cDNA DKFZp586E2023 (from clone DKFZp586E2023) /cds=UNKNOWN /gb=AL050202 /gi=4884441 /ug=Hs.29005 /len=1169	1.960259397	0.00553
34778_at	Cluster Incl AA418080:zv97h07.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-767773 /clone_end=3" /gb=AA418080 /gi=2079881 /ug=Hs.3972 /len=543	1.974272775	0.015166
37147_at	Cluster Incl AF020044:Homo sapiens lymphocyte secreted C-type lectin precursor, mRNA, complete cds /cds=(179,1150) /gb=AF020044 /gi=2828595 /ug=Hs.105927 /len=1391	2.009944208	0.007262
41405_at	Cluster Incl AF026692:Homo sapiens frizzled related protein frpHE mRNA, complete cds /cds=(257,1297) /gb=AF026692 /gi=2920803 /ug=Hs.105700 /len=2840	2.176388814	0.011092
38637_at	Cluster Incl L16895:Human lysyl oxidase (LOX) gene, exon 7 /cds=(0,6) /gb=L16895 /gi=292923 /ug=Hs.102267 /len=2052	2.180657934	0.034442
1114_at	M22490 /FEATURE= /DEFINITION=HUMBMP2B Human bone morphogenetic protein-2B (BMP-2B) mRNA	2.23232076	0.013214
671_at	J03040 /FEATURE= /DEFINITION=HUMSPARC Human SPARC/osteonectin mRNA, complete cds	2.271250535	0.007548
652_g_at	L07493 /FEATURE= /DEFINITION=HUM14RPA Homo sapiens replication protein A 14kDa subunit (RPA) mRNA, complete cds	2.271349484	0.001554
41169_at	Cluster Incl X74039:H.sapiens mRNA for urokinase plasminogen activator receptor /cds=(46,891) /gb=X74039 /gi=456192 /ug=Hs.179657 /len=1070	2.278539606	0.023709
39710_at	Cluster Incl U30521:Human P311 HUM (3.1) mRNA, complete cds /cds=(202,408) /gb=U30521 /gi=963091 /ug=Hs.142827 /len=2036	2.338829553	0.004316
38466_at	Cluster Incl X82153:H.sapiens mRNA for cathepsin O /cds=(129,1118) /gb=X82153 /gi=562756 /ug=Hs.83942 /len=1669	2.362505408	0.002649
36007_at	Cluster Incl AL050137:Homo sapiens mRNA; cDNA DKFZp586L151 (from clone DKFZp586L151) /cds=(0,1300) /gb=AL050137 /gi=4884149 /ug=Hs.43658 /len=1810	2.433041892	0.013328

Table 7. Genes present in the U95_A cluster which are not in the Fold Change list (>1 over-expressed in Barrett's-associated esophageal denocarcinoma (BA), <1 under-expressed in BA)

Affy ID	Gene Name	Fold Change	P-value
41870_at	Cluster Incl AF030428:Homo sapiens lung type-I cell membrane-associated protein hT1a-2 (hT1a-2) mRNA, complete cds /cds=(180,668) /gb=AF030428 /gi=4103968 /ug=Hs.135150 /len=865	2.540477039	0.017889
39271_at	Cluster Incl AA461365:zx70e07.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-796836 /clone_end=5" /gb=AA461365 /gi=2186485 /ug=Hs.237742 /len=591"	2.588708014	0.020462
37678_at	Cluster Incl U23070:Human putative transmembrane protein (nma) mRNA, complete cds /cds=(372,1154) /gb=U23070 /gi=1262172 /ug=Hs.78776 /len=1521	2.591572193	0.005203
37906_at	Cluster Incl Z37976:H.sapiens mRNA for latent transforming growth factor-beta binding protein (LTBP-2) /cds=(388,583) /gb=Z37976 /gi=1272663 /ug=Hs.83337 /len=7000	2.599655226	0.001094
40681_at	Cluster Incl AB008375:Homo sapiens mRNA for osteoblast specific cysteine-rich protein, complete cds /cds=(378,1589) /gb=AB008375 /gi=2570151 /ug=Hs.82582 /len=2375	2.647250803	0.006876
34862_at	Cluster Incl AA005018:zh96a09.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-429112 /clone_end=5" /gb=AA005018 /gi=1448859 /ug=Hs.4963 /len=637"	2.87530968	0.002292
38112_g	Cluster Incl X15998:H.sapiens mRNA for the chondroitin sulphate proteoglycan versican, V1 splice-variant; precursor peptide /cds=(266,7495) /gb=X15998 /gi=37662 /ug=Hs.81800 /len=8224	2.907786251	0.015823
32617_at	Cluster Incl W74442:zd75e09.s1 Homo sapiens cDNA, 3 end /clone=IMAGE-346504 /clone_end=3" /gb=W74442 /gi=1384777 /ug=Hs.80961 /len=580"	1.863661777	0.014302
35479_at	Cluster Incl AJ242015:Homo sapiens mRNA for eMDC II protein /cds=(47,2374) /gb=AJ242015 /gi=4757043 /ug=Hs.174030 /len=3056	2.399523898	0.010738
33168_at	Cluster Incl H24861:y42e11.r1 Homo sapiens cDNA, 5 end /clone=IMAGE-160940 /clone_end=5" /gb=H24861 /gi=893760 /ug=Hs.90145 /len=517"	2.450031618	0.000099
37821_at	Cluster Incl AF041260:Homo sapiens AIBC1 (AIBC1) mRNA, complete cds /cds=(117,1871) /gb=AF041260 /gi=3335398 /ug=Hs.129057 /len=2813	2.641191847	0.03309
34830_at	Cluster Incl W25986:17e7 Homo sapiens cDNA /gb=W25986 /gi=1306253 /ug=Hs.4750 /len=769	2.743466262	0.000057
35724_at	Cluster Incl Y07867:H.sapiens mRNA for Pirin, isolate 1 /cds=(204,1076) /gb=Y07867 /gi=1907075 /ug=Hs.38842 /len=1277	0.390677117	0.000031
1779_s_at	M16750 /FEATURE= /DEFINITION=HUMPM1 Human pim-1 oncogene mRNA, complete cds	0.361169226	0.000229
37533_r_a	Cluster Incl D86980:Human mRNA for KIAA0227 gene, partial cds /cds=(0,1011) /gb=D86980 /gi=1504033 /ug=Hs.79170 /len=5217	0.358908632	0.000665

Table 7. Genes present in the U95_A cluster which are not in the Fold Change list (>1 over-expressed in Barrett's-associated esophageal denocarcinoma (BA), <1 under-expressed in BA)

Affy ID	Gene Name	Fold Change	P-value
38553_r_a	Cluster Incl AI984786:wr85c06.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-2494474 /clone_end=3" /gb=AI984786 /gi=5812063 /ug=Hs.175941 /len=814"	0.354417702	0.000137
38349_at	Cluster Incl AF038564:Homo sapiens atrophin-1 interacting protein 4 (AIP4) mRNA, partial cds /cds=(0,2219) /gb=AF038564 /gi=2708328 /ug=Hs.98074 /len=2358	0.351660122	0.000684
37596_at	Cluster Incl U09117:Human phospholipase c delta 1 mRNA, complete cds /cds=(94,2364) /gb=U09117 /gi=483919 /ug=Hs.80776 /len=2627	0.351047496	0.001325
34931_at	Cluster Incl AB023157:Homo sapiens mRNA for KIAA0940 protein, complete cds /cds=(89,2143) /gb=AB023157 /gi=4589523 /ug=Hs.131945 /len=5715	0.350176398	0.000066
36116_at	Cluster Incl AJ000414:Homo sapiens mRNA for Cdc42-interacting protein 4 (CIP4) /cds=(39,1676) /gb=AJ000414 /gi=2274965 /ug=Hs.73999 /len=2001	0.346256072	0.00077
37217_at	Cluster Incl AI208485:qg36f11.x1 Homo sapiens cDNA, 3 end /clone=IMAGE-1837293 /clone_end=3" /gb=AI208485 /gi=3770427 /ug=Hs.77253 /len=537"	0.337140887	0.000001

Table 8. Genes identified by heirarchical clustering of the full Human Genome U95 set showing fold change between normal and diseased sample sets.

ACCESSION	FOLD CHANGE	NAME
AI199897	-22.0	EST
W69365	-8.2	EST
AI081571	-8.9	EST
AI962905	-9.6	CGI-119 PROTEIN
AI885390	-8.6	EST
X94323	-11.2	SPECIFIC GRANULE PROTEIN
M62982	-11.4	ARACHIDONATE 12-LIPOXYGENASE
X87159	-6.5	SODIUM CHANNEL (SCNNIB)
M32402	-9.7	PLACENTA PROTEIN 11
AI739630	-19.7	EST
AW025309	-40.5	EST
AB001325	-20.2	AQUAPORIN 3
AI582193	-35.1	EST
AB002134	-12.1	AIRWAY TRYPSIN-LIKE PROTEASE
AL050220	-17.6	KALLIKREIN 13
AI971202	-12.2	EST
AI669212	-14.3	EST
AI916261	-9.2	EST
M24902	-1.0	ACID PHOSPHATASE PROSTATE
U83115	-8.1	AIM1 (ABSENT IN MELANOMA)
Y09538	-17.3	ZINC FINGER PROTEIN 185
AI142832	-15.4	EST
Y16961	-12.6	TUMOR PROTEIN P63
AA130221	-22.4	EST
AA781220	-19.0	PAIRED BOX GENE 9 (PAX9)
AI282714	-77.6	DESCI PROTEIN
M98477	-22.2	TRANSGLUTAMINASE 1
AI540870	-27.6	EST
AF045941	-24.5	SCIELLIN
R37637	-44.5	EST
AA743820	-49.5	EST
AI623978	-03.1	EST
AI859619	-15.9	EST
AJ223693	-10.5	GPI-ANCHORED HOMOLOG
AI378979	-37.1	KATANIN P60 SUBUNIT A1
S66896	-14.2	SCCAI
W68630	-28.5	EST
AA401397	-16.4	KATANIN 13
AA010777	-35.7	GALECTIN 7
L10386	-25.1	TRANSGLUTAMINASE 3
A1814274	-123.8	EST
X76342	-20.7	ALCOHOL DEHYDROGENASE 7

Table 8. Genes identified by heirarchical clustering of the full Human Genome U95 set showing fold change between normal and diseased sample sets.

AI692575	-46.0	EST
ACCESSION	FOLD CHANGE	NAME
T71258	-23.9	?
AI265958	-58.2	EST
M13903	-15.7	INVOLUCRIN
M60047	-20.7	HBP17
X99977	-35.3	ARS GENE, COMPONENT B
AI369347	-7.9	EST
A1052020	-7.4	EST
AI818579	2.5	EST
AI557210	4.7	EST
AI754693	4.1	EST
AB029000	8.3	MRNA FOR KIAA1077 PROTEIN
U09278	7.9	FIBROBLAST ACTIVATION PROTEIN, ALPHA
AA044844	3.4	SOLUTE CARRIER FAMILY 11, MEMBER 3
J04162	3.1	Fc FRAGMENT OF IgC, LOW AFFINITY IIIA
AA147884	5.0	EST
AA584310	13.2	CGI-101 PROTEIN
D21254	3.8	CADHERIN-11
D21255	3.9	CADHERIN-11
X82153	2.4	CATHEPSIN K
AA127736	3.6	COLLAGEN, TYPE V, ALPHA 2
AW007442	6.4	BIGLYCAN
Z37976	2.6	LATENT TGF β BINDING PROTEIN 2
AI686894	3.5	EST
AA007367	6.6	EST
AF052124	9.5	SPPI (OSTEOPONTIN)
AA088177	4.3	EST
J04765	5.4	SPPI (OSTEOPONTIN)
AA447232	4.3	CATHEPSIN B
X15998	4.3	CHONDROITIN SULFATE PROTEOGLYCAN 2
AA426499	3.8	CHONDROITIN SULFATE PROTEOGLYCAN 2
X15998	2.9	CHONDROITIN SULFATE PROTEOGLYCAN 2
AA704137	5.4	THY-1 CELL SURFACE ANTIGEN
AI740961	5.7	EST
AI864014	17.2	SPPI (OSTEOPONTIN)
D13666	5.0	OSTEOBLAST SPECIFIC FACTOR 2
AL050137	3.1	EST
AI970896	3.1	EST
AF020044	2.0	STEM CELL GROWTH FACTOR
AI333224	3.0	EST
AI091277	3.9	EST
W74476	4.7	EST
AA056278	5.3	EHM2 GENE

Table 8. Genes identified by heirarchical clustering of the full Human Genome U95 set showing fold change between normal and diseased sample sets.

AA877900	20.3	HYPOTHETICAL PROTEIN FLJ20063
AI799626	10.2	EST
ACCESSION	FOLD CHANGE	NAME
M35252	33.9	TRANSMEMBRANE, 4, SUPERFAMILY MEMBER 3
AI961220	30.1	SERINE PROTEASE INHIBITOR (SPINK1)
AI148745	9.6	EST
AI982768	5.7	EST
H30385	4.8	EST
AB023171	10.6	MRNA FOR KIAA0954 PROTEIN
AW007803	7.4	EST
AA458524	7.5	EST
AI301060	9.0	EST
AI859849	16.2	EST
AA156240	5.9	SERINE PROTEASE, UMBLICAL ENDOTHELIUM
AI691066	15.8	EST
AB006781	20.9	GALECTIN 4
AA535447	18.6	EST
AI125252	15.9	EST
AI308063	126.9	EST
U73167	4.3	COSMID CLONE
N30008	3.8	EST
AI392817	5.6	HEPATOCYTE NUCLEAR FACTOR 3 GAMMA
AB018335	5.2	MRNA FOR KIAA0792 PROTEIN
AF065388	5.3	TETRASPAN-1

What is claimed is:

1. A method of diagnosing esophageal cancer in a patient, comprising:

5 (a) detecting the level of expression in a tissue sample of two or more genes from
Tables 2-8; wherein differential expression of the genes in Tables 2-8 is indicative of
esophageal cancer.

2. A method of detecting the progression of esophageal cancer in a patient,
comprising:

10 (a) detecting the level of expression in a tissue sample of two or more genes from
Tables 2-8; wherein differential expression of the genes in Tables 2-8 is indicative of
esophageal cancer progression.

3. A method according to claim 2, wherein the progression is the progression of
15 Barrett's esophagus to adenocarcinoma.

4. A method of monitoring the treatment of a patient with esophageal cancer,
comprising:

(a) administering a pharmaceutical composition to the patient;
20 (b) preparing a gene expression profile from a cell or tissue sample from the patient;
and
(c) comparing the patient gene expression profile to a gene expression from a cell
population selected from the group consisting of normal esophageal cells, cells from Barrett's
esophagus and esophageal adenocarcinoma cells.

25

5. A method of treating a patient with esophageal cancer, comprising:

(a) administering to the patient a pharmaceutical composition, wherein the
composition alters the expression of at least one gene in Tables 2-8;

(b) preparing a gene expression profile from a cell or tissue sample from the patient
30 comprising esophageal cancer cells; and

(c) comparing the patient expression profile to a gene expression profile selected from the group consisting of normal esophageal cells, cells from Barrett's esophagus and esophageal adenocarcinoma cells.

5 6. A method of diagnosing esophageal adenocarcinoma in a patient, comprising:

(a) detecting the level of expression in a tissue sample of two or more genes from Tables 2-8; wherein differential expression of the genes in Tables 2-8 is indicative of esophageal adenocarcinoma.

10 7. A method of detecting the progression of esophageal adenocarcinoma in a patient, comprising:

(a) detecting the level of expression in a tissue sample of two or more genes from Tables 2-8; wherein differential expression of the genes in Tables 2-8 is indicative of esophageal adenocarcinoma progression.

15

8. A method of monitoring the treatment of a patient with esophageal adenocarcinoma, comprising:

(a) administering a pharmaceutical composition to the patient;

(b) preparing a gene expression profile from a cell or tissue sample from the patient;

20 and

(c) comparing the patient gene expression profile to a gene expression from a cell population comprising normal esophageal cells or to a gene expression profile from a cell population comprising esophageal adenocarcinoma cells or to both.

25 9. A method of treating a patient with esophageal adenocarcinoma, comprising:

(a) administering to the patient a pharmaceutical composition, wherein the composition alters the expression of at least one gene in Tables 2-8;

(b) preparing a gene expression profile from a cell or tissue sample from the patient comprising esophageal adenocarcinoma cells; and

30

(c) comparing the patient expression profile to a gene expression profile from an untreated cell population comprising esophageal adenocarcinoma cells.

10. A method of screening for an agent capable of modulating the onset or progression of esophageal cancer, comprising:

(a) preparing a first gene expression profile of a cell population comprising esophageal cancer cells, wherein the expression profile determines the expression level of one
5 or more genes from Tables 2-8;

(b) exposing the cell population to the agent;

(c) preparing second gene expression profile of the agent-exposed cell population; and

(d) comparing the first and second gene expression profiles.

10 11. The method of claim 14, wherein the esophageal cancer is a esophageal adenocarcinoma.

12. A composition comprising at least two oligonucleotides, wherein each of the oligonucleotides comprises a sequence that specifically hybridizes to a gene in Tables 2-8.

15

13. A composition according to claim 12, wherein the composition comprises at least 3 oligonucleotides.

14. A composition according to claim 12, wherein the composition comprises at least
20 5 oligonucleotides.

15. A composition according to claim 12, wherein the composition comprises at least 7 oligonucleotides.

25 16. A composition according to claim 12, wherein the composition comprises at least 10 oligonucleotides.

17. A composition according to any one of claims 12-16, wherein the oligonucleotides are attached to a solid support.

30

18. A composition according to claim 17, wherein the solid support is selected from a group consisting of a membrane, a glass support, a filter, a tissue culture dish, a polymeric material, a bead and a silica support.

5 19. A solid support comprising at least two oligonucleotides, wherein each of the oligonucleotides comprises a sequence that specifically hybridizes to a gene in Tables 2-8.

20. A solid support according to claim 19, wherein the oligonucleotides are covalently attached to the solid support.

10 21. A solid support according to claim 20, wherein the oligonucleotides are non-covalently attached to the solid support.

22. A solid support according to claim 19, wherein the support comprises at least
15 about 10 different oligonucleotides in discrete locations per square centimeter.

23. A solid support according to claim 19, wherein the support comprises at least about 100 different oligonucleotides in discrete locations per square centimeter.

20 24. A solid support according to claim 19, wherein the support comprises at least about 1000 different oligonucleotides in discrete locations per square centimeter.

25. A solid support according to claim 19, wherein the support comprises at least about 10,000 different oligonucleotides in discrete locations per square centimeter.

25 26. A computer system comprising:
(a) a database containing information identifying the expression level in esophageal tissue of a set of genes comprising at least two genes in Tables 2-8; and
(b) a user interface to view the information.

30 26. A computer system of claim 25, wherein the database further comprises sequence information for the genes.

27. A computer system of claim 25, wherein the database further comprises information identifying the expression level for the set of genes in normal esophageal tissue.

5 28. A computer system of claim 25, wherein the database further comprises information identifying the expression level of the set of genes in esophageal cancer tissue.

29. A computer system of claim 28, wherein the esophageal cancer tissue comprises esophageal adenocarcinoma cells.

10 30. A computer system of claim 31-36, further comprising records including descriptive information from an external database, which information correlates said genes to records in the external database.

15 31. A computer system of claim 30, wherein the external database is GenBank.

32. A method of using a computer system of any one of claims 26-29 to present information identifying the expression level in a tissue or cell of at least one gene in Tables 2-8, comprising:

20 (a) comparing the expression level of at least one gene in Tables 2-8 in the tissue or cell to the level of expression of the gene in the database.

33. A method of claim 32, wherein the expression level of at least two genes are compared.

25 34. A method of claim 32, wherein the expression level of at least five genes are compared.

35. A method of claim 32, wherein the expression level of at least ten genes are
30 compared.

36. A method of claim 32, further comprising displaying the level of expression of at least one gene in the tissue or cell sample compared to the expression level in esophageal cancer.

AMENDED CLAIMS

[received by the International Bureau on 2 October 2001 (02.10.01);
original claims 11, 21 and 27-36 amended; remaining claims unchanged (4 pages)]

10. A method of screening for an agent capable of modulating the onset or progression of esophageal cancer, comprising:
- (a) preparing a first gene expression profile of a cell population comprising esophageal cancer cells, wherein the expression profile determines the expression level of one or more genes from Tables 2-8;
 - (b) exposing the cell population to the agent;
 - (c) preparing second gene expression profile of the agent-exposed cell population; and
 - (d) comparing the first and second gene expression profiles.
11. The method of claim 10, wherein the esophageal cancer is a esophageal adenocarcinoma.
12. A composition comprising at least two oligonucleotides, wherein each of the oligonucleotides comprises a sequence that specifically hybridizes to a gene in Tables 2-8.
13. A composition according to claim 12, wherein the composition comprises at least 3 oligonucleotides.
14. A composition according to claim 12, wherein the composition comprises at least 5 oligonucleotides.
15. A composition according to claim 12, wherein the composition comprises at least 7 oligonucleotides.
16. A composition according to claim 12, wherein the composition comprises at least 10 oligonucleotides.
17. A composition according to any one of claims 12-16, wherein the oligonucleotides are attached to a solid support.

18. A composition according to claim 17, wherein the solid support is selected from a group consisting of a membrane, a glass support, a filter, a tissue culture dish, a polymeric material, a bead and a silica support.

19. A solid support comprising at least two oligonucleotides, wherein each of the oligonucleotides comprises a sequence that specifically hybridizes to a gene in Tables 2-8.

20. A solid support according to claim 19, wherein the oligonucleotides are covalently attached to the solid support.

21. A solid support according to claim 19, wherein the oligonucleotides are non-covalently attached to the solid support.

22. A solid support according to claim 19, wherein the support comprises at least about 10 different oligonucleotides in discrete locations per square centimeter.

23. A solid support according to claim 19, wherein the support comprises at least about 100 different oligonucleotides in discrete locations per square centimeter.

24. A solid support according to claim 19, wherein the support comprises at least about 1000 different oligonucleotides in discrete locations per square centimeter.

25. A solid support according to claim 19, wherein the support comprises at least about 10,000 different oligonucleotides in discrete locations per square centimeter.

26. A computer system comprising:

- (a) a database containing information identifying the expression level in esophageal tissue of a set of genes comprising at least two genes in Tables 2-8; and
- (b) a user interface to view the information.

27. A computer system of claim 26, wherein the database further comprises sequence information for the genes.

28. A computer system of claim 26, wherein the database further comprises information identifying the expression level for the set of genes in normal esophageal tissue.

29. A computer system of claim 26, wherein the database further comprises information identifying the expression level of the set of genes in esophageal cancer tissue.

30. A computer system of claim 29, wherein the esophageal cancer tissue comprises esophageal adenocarcinoma cells.

31. A computer system of claim 26-30, further comprising records including descriptive information from an external database, which information correlates said genes to records in the external database.

32. A computer system of claim 31, wherein the external database is GenBank.

33. A method of using a computer system of any one of claims 26-30 to present information identifying the expression level in a tissue or cell of at least one gene in Tables 2-8, comprising:

(a) comparing the expression level of at least one gene in Tables 2-8 in the tissue or cell to the level of expression of the gene in the database.

34. A method of claim 33, wherein the expression level of at least two genes are compared.

35. A method of claim 33, wherein the expression level of at least five genes are compared.

36. A method of claim 33, wherein the expression level of at least ten genes are compared.

37. A method of claim 33, further comprising displaying the level of expression of at least one gene in the tissue or cell sample compared to the expression level in esophageal cancer.

STATEMENT UNDER PCT ARTICLE 19(1)

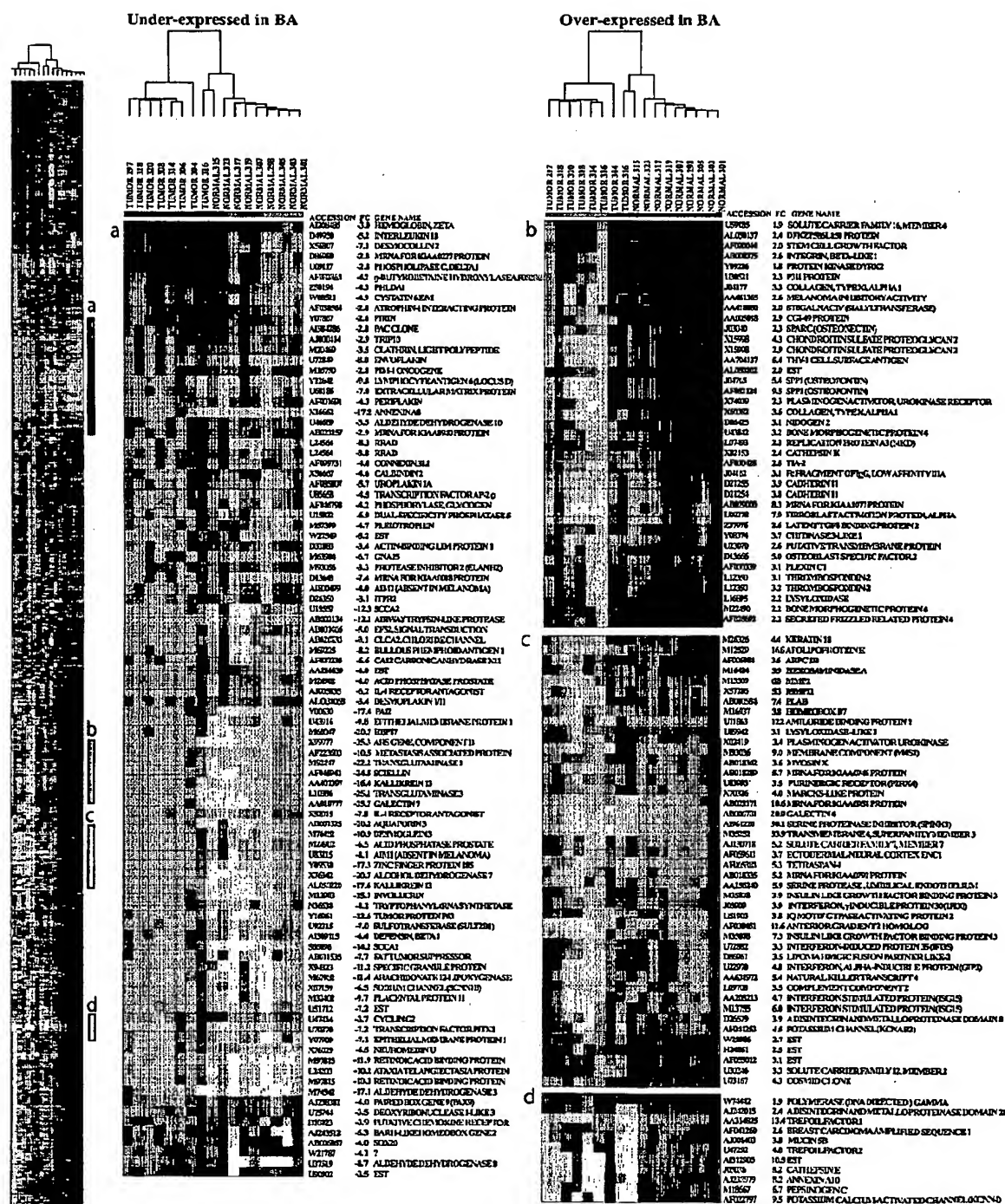
Applicants herewith submit replacement sheets numbered 158-161 to replace sheets numbered 158-161 as originally filed on 28 March 2001 at the U.S. Receiving Office (RO/US).

With respect to each claim appearing in the international application based on the replacement sheets submitted herewith, and in accordance with PCT Section 205, the following claims are:

unchanged:	claim(s) <u>10, 12-17, 18-20, and 22-26</u>
canceled:	claim(s) <u>none</u>
new:	claim(s) <u>none</u>

Applicants have amended claims 11, 21, and 27-36 to correct the claim numbering and the dependencies of the renumbered claims. The amendment does not go beyond the disclosure as originally filed.

Applicants request entry of the amendment and publication of PCT/US01/09847 with the amended claims.



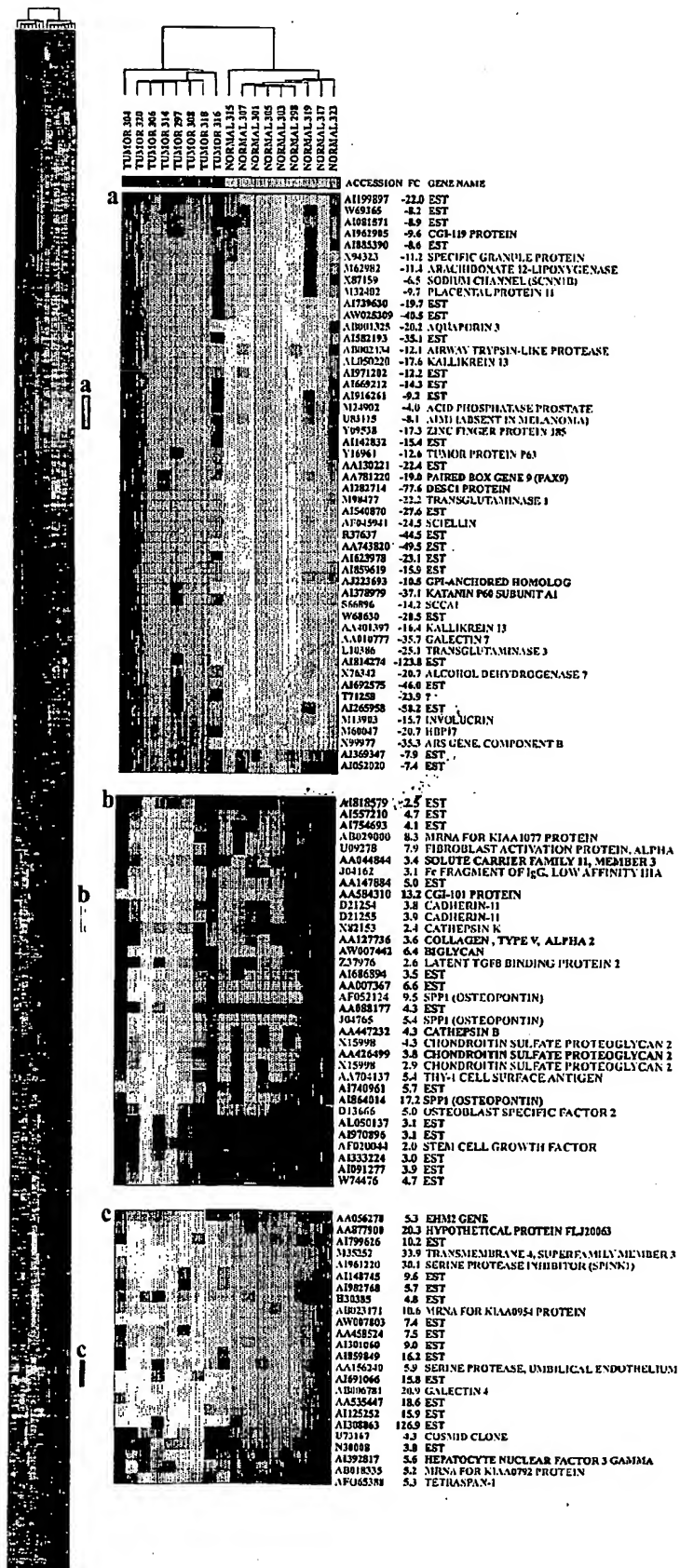


Figure 2

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US01/09847

A. CLASSIFICATION OF SUBJECT MATTER

IPC(7) : A61K 48/00
US CL : 514/44; 424/93.1

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
U.S. : 514/44; 424/93.1

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)
Please See Continuation Sheet

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A, P	ISHII, H. et al. Effect of Adenoviral Transduciton of the Fragile Histidine Triad Gene into Esophageal Cancer Cells. Cancer Research. 15 February 2001, Vol. 61.	1-11
A	WO 98/33527 B2 (COHEN et al) 06 August 1998 (06.08.1998).	1-11
A, P	US 6,229,911 B1 (BALABAN et al) 08 May 2001 (08.05.2001).	26-36
A	US 5,824,485 A (THOMPSON et al) 20 October 1998 (20.10.1998).	26-36

☐ Further documents are listed in the continuation of Box C.

☐ See patent family annex.

Special categories of cited documents:	
"A" document defining the general state of the art which is not considered to be of particular relevance	"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
"E" earlier application or patent published on or after the international filing date	"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
"O" document referring to an oral disclosure, use, exhibition or other means	"&" document member of the same patent family
"P" document published prior to the international filing date but later than the priority date claimed	

Date of the actual completion of the international search

12 June 2001 (12.06.2001)

Date of mailing of the international search report

02 AUG 2001

Name and mailing address of the ISA/US

Commissioner of Patents and Trademarks
Box PCT
Washington, D.C. 20231

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Konstantina Katchaves

Telephone No. (703) 308-0196

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US01/09847

Box I Observations where certain claims were found unsearchable (Continuation of Item 1 of first sheet)

This international report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claim Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

2. ☒ Claim Nos.: 12-25
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:
Claims 12-25 are drawn to sequences provided in the tables. However, Applicant has failed to provide a computer readable copy of the claimed sequences so that a proper search can be conducted.

3. ☐ Claim Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of Item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:

4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

☐
☐

- The additional search fees were accompanied by the applicant's protest.
No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT

International application No.

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Continuation of B. FIELDS SEARCHED Item 3: EAST, STN, MEDLINE, CAPLUS, EMBASE

Search terms: treat, inhibit, detect, esophageal cancer, screen, database, bioinformatics